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**FIGURE 8**

MAAIPDSWQPPNVYLETSMGIIVLELYWKHAPKTCKNFAELARRGYNGTKFHRIIKDFMIQ  
GGDPTGTGRGGASIYGKQFEDELHPDLKFTGAGILAMANAGPDTNGSQFFVTLPQTQWLDGKH  
TIFGRVCQGIGMVNRVGMVETNSQDRPVDDVKIIKAYPSG

**Important features:****N-glycosylation sites:**

amino acids 49-52, 108-111

**N-myristoylation sites:**

amino acids 64-69, 69-74, 143-148

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature:**

amino acids 48-65

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## FIGURE 9

[illegible]

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**FIGURE 10**

MWHEARKHERKLRGMMVDYKKRAERRREYYEKIKKDPAQFLQVHGRACKVHLDLSAVALAAESP  
 VNMMPWQGDNTNNMIDRFVRAHLHDHIDYTPPLTTISPEQESDERKCNERYRGLVQNDFAG  
 ISEEQCLYQIYIDELYGGLQRPSEDEKKKLAEEKASIGTYEDSTVAEVEKAAEKPEEEESAA  
 EEESNDEDEVIPIIDVEVDVDVDELNQEQVADLNKQATTYGMADGDFVRLRKDKKEEAETKHA  
 KALEEEKAMYSGRRSRRQRREFREKRLRGRKISPPSYARRDSPTYDPYKRSPSESSSESRSRS  
 RSPTPGREEKITFITSFGGSDEEAAAAAAAAASGVTTGKPPAFPQGGPAPGRNASARRRSS  
 SSSSSSSASRTSSSRSSSRSSSRSSRRGGGYRSGRHARSRSRSWSRSRSRSRRYSRSRSRGRR  
 HSGGGSRDGHRYSRSPARRGGYGPRRRSRSRSHSGDRYRGGRLRHSSSSRSRSSWSLSPSR  
 SRSLSRSHSPSPSQSRSRSRSSQSPSPSPAREKLTTPAASPAVGEKLLKTEPAAGKETGA  
 AKVTQADASGEAETEDAEGAEQAVQGG

**Important features:****N-glycosylation site:**

amino acids 370-373

**Glycosaminoglycan attachment site:**

amino acids 443-446

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**amino acids 159-162, 282-285, 291-294, 374-377, 375-378, 430-433,  
440-443, 466-469**Casein kinase II phosphorylation site:**amino acids 149-152, 166-169, 171-174, 187-190, 193-196, 195-198,  
303-306, 307-310, 335-338, 571-574**N-myristoylation sites:**

amino acids 118-123, 229-234, 350-355, 446-451, 586-591

**Amidation sites:**

amino acids 263-266, 280-283, 438-441

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**FIGURE 11**

GGTAGGCGCGCCAGACCTGAGACGGGTGGGACTGGGCTGCGTCACGCGCGGGCTCTAAGCG  
CCCGGGGCCCGCCAGTGCGCGGCACAGCCAATCGCAGCGCGGGAAGGCGGTGGGGCGGGG  
AAGGCGCGCTGGAAACTTAAATCCCGAGGCGGGCGAACTGCACCAGACCGCGGAGCTGTGTA  
ATCTCAGAGGCTTGTTTGCTGAGGGTGCCTGCGCAGCTGCGACGGCTGCTGGTTTTGAAACAT  
GAATCTTTCGCTCGTCCCTGGCTGCCTTTTGCTTGGGAATAGCCTCCGCTGTTCCAAAATTTGA  
CCAAAATTTGGATACAAAGTGGTACCACTGGAAGGCAACACACAGAAGATTATATGGCGCGAA  
TGAAGAAGGATGGAGGAGAGCAGTGTGGGAAAAGAATATGAAATGATTGAACTGCACAATGG  
GGAATACAGCCAAGGGAACATGGCTTCACAATGGCCATGAATGCTTTTGGTGACATGACCAA  
TGAAGAATTCAAGGAGATGATGGGTTGCTTTCGAAACCAGAAATTCAGGAAGGGGAAAGTGTT  
CCGTGAGCCTCTGTTTCTTGATCTTCCCAAATCTGTGGATTGGAGAAAGAAAGGCTACGTGAC  
GCCAGTGAAGAATCAGAAACAGTGTGGTTCTTGTTGGGCTTTTAGTGCAGCTGGTGCTCTTGA  
AGGACAGATGTTCCGGAAAACCTGGGAACTTGCTCACTGAGCGAGCAGAATCTGGTGGACTG  
TTCGCGTCCCAAGGCAATCAGGGCTGCAATGGTGGCTTCATGGCTAGGGCCTTCCAGTATGT  
CAAGGAGAACGGAGGCCCTGGACTCTGAGGAATCCTATCCATATGTAGCAGTGGATGAAATCTG  
TAAGTACAGACCTGAGAATTCTGTTGCTAATGACACTGGCTTCACAGTGGTCGCACCTGGAAA  
GGAGAAGGCCCTGATGAAAGCAGTCGCAACTGTGGGGCCCATCTCCGTGCTATGGATGCAGG  
CCATTTCGTCTTCCAGTTCTACAAAATCAGGCATTTATTTTGAACCAGACTGCAGCAGCAAAAA  
CCTGGATCATGGTGTCTGGTGGTTGGCTACGGCTTTGAAGGAGCAAATTCGAATAACAGCAA  
GTATTGGCTCGTCAAAAAACAGCTGGGGTCCAGAATGGGGCTCGAATGGCTATGTAAAAATAGC  
CAAAGACAAGAACAACCACTGTGGAATCGCCACAGCAGCCAGCTACCCCAATGTGTCAGCTGA  
TGGATGGTGAGGAGGAAGGACTTAAGGACAGCATGTCTGGGAAATTTTATCTTGAAACTGAC  
CAAACGCTTATTGTGTAAGATAAACCAGTTGAATCATGGAGGATCCAAGTTGAGATTTTAATT  
CTGTGACATTTTTACAAGGGTAAAAATGTTACCACTACTTTAATTATGTGTATACACAGCTTTA  
TGATATCAAAGACTCATTGCTTAATTCTAAGACTTTTGAATTTTCATTTTTTAAAAAGATGTA  
CAAAACAGTTTGAATAAATTTTAATTCGTATATA

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**FIGURE 12**

MNLSLVLA AFCLGIASAVPKFDQNLDTKWYQWKATHRRLYGANEEGWRRRAVWEKNMKMIELHN  
GEYSQKGKHGFTMAMNAFGDMTNEEFQMMGCFRNQKFRKGKVFREPLFLDLPKSVDWRRKKGYV  
TPVKNQKQCGSCWAFSATGALEGQMFRTGKLVSLSEQNLVDCSRPQGNQGCNGGFMARAFQY  
VKENGGLDSEESYPYVAVDEICKYRPENSVANDTGFTVVPAGKEKALMKAVATVGPISVAMDA  
GHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEGANSNNKYWLVKNSWGP EWGSNGYVKI  
AKDKNNHCGIATAASYPNV

**Important features:****Signal sequence**

amino acids 1-17

**N-glycosylation sites.**

amino acids 2-6, 221-225, 292-296

**N-myristoylation sites.**amino acids 13-19, 93-99, 136-142, 145-151, 174-180, 177-183,  
180-186, 194-200, 288-294, 324-330**Eukaryotic thiol (cysteine) proteases cysteine active site.**

amino acids 132-144

**Eukaryotic thiol (cysteine) proteases histidine active site.**

amino acids 275-286

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**FIGURE 13**

GGCGCGCTCATGTGATCCGCTTCCCTGCTCCTTTAAGCGTCCACAGGCGCGGAGCGGCCACA  
ATCAGAGCTCCGGGCATTGGGGGAACCCGAGCCGGCTGCGCCGGGGGAATCCGTGCGGGCGCC  
TTCGCTCCCGGTCCCATCTCTCGCCGCGCTCCAGCACCTCTGAAGTTTTGACAGCGCCAGAAAG  
GAGGCGAGGAAGGAGGGAGTGTGTGAGAGGAGGAGCAAAAAGCTCACCCTAAAAACATTATT  
TCAAGGAGAAAAAGAAAAGGGGGGGCGCAAAAATGGCTGGGGCAATTATAGAAAACATGAGCA  
CCAAGAGCTGTGCATTGTTGGTGGGATTTCGCTCGTGTCCAAATCATCGCCTTTCTGGTGG  
GAGGCTTGATTGCTCCAGGTCACAAAGGCCACAAACGGCAGTGTCTACATGTCGGTGAATGTGTGGATG  
CCCGTAAGAACCATCACAAGACAAAATGGTTCGTGCCTTGGGGACCCAAATCATTGTGACAAGA  
TCCGAGACATTTGAAGAGGCAATTCCAAGGGAATGAAGCCAATGACATCGTGTCTCTGTTC  
ACATTCCCTCCCCACATGGAGATGAGTCTTGGTCCAATTCAATGCTGTTTACTCTGCAGC  
TGGACATTGCCTTCAAGCTAAACAACCAAAATCAGAGAAAATGCAGAAGTCTCCATGGACGTTT  
CCCTGGCTTACCGTGATGACGCATTTGCTGAGTGGACTGAAATGGCCCATGAAAGAGTACCAC  
GGAAACTCAAATGCACCTTACATCTCCCAAGACTCCAGAGCATGAGGGCCGTTACTATGAAT  
GTGATGTCCTTCCCTTTCATGGAATTTGGGTCTGTGGCCCATAGTTTTACCTTTTAAACATCC  
GGCTGCGCTGTGAATGAGAGAAGAAAATCAATGTGGGAATTTGGGGAGATAAAGGATATCCGGT  
TGGTGGGGAATCCACCAAGGTGGAGGCTTCCCAAGGTGTGGTTTGGCATGAAGACCTTCCTTA  
CGCCAGCATCTTCATCATTATGGTGTGGTATTGGAGGAGGATCACCATGATGTCCCGACCCC  
CAGTGTCTTGGAAAAAGTCATCTTTGCCCTTGGGATTTCATGACCTTTATCAATATCCCGAG  
TGAATTTGGTTTTCATCGGTTTGGACTGGACCTGGATGCTGCTGTTTGGTGACATCCGACAGG  
GCATCTTCTATGCGATGCTTCTGTCTTCTGGATCATCTCTGTGGCGAGCAGATGATGGATC  
AGCAGGAGCGGAACCATCGCAGGGTATTGGAAGCAAGTCGGACCCATTGCCGTTGGCTCCT  
TCTGCCCTTTCATATTTGACATGTGTGAGAGAGGGGTACAATCAGCAATCCCTTACAGTA  
TCTGGACTACAGACATTGGAACAGAGCTGGCCATGGCCTTCATCATCGTGGCTGGAATCTGCC  
TCTGCCCTCTACTTCCCTGTTTCTATGCTTTCATGGTATTTCAAGTGTTCGGAACATCAGTGGGA  
AGCAGTCCAGCTGCCAGCTATGAGCAAAGTCCGGCGGCTACACATGAGGGGCTAATTTTTTA  
GGTTCAAGTTCCTCATGCTTATCACCTTGGCCTGCGCTGCCATGACTGTCACTTCTTTCATCG  
TTAGTCAGGTAACGGAAGGCCATTGGAATGGGCGGCGCTCACAGTCCAAGTGAACAGTGCCT  
TTTTACAGGCATCTATGGGATGTGGAATCTGTATGCTTTGGTCTGATGTTCTTGTATGCAC  
CATCCCATAAAACTATGGAGAAGACCAAGTCCAATGGCGATCTGGGTGTCCATAGTGGGGAAG  
AACTCCAGCTCACCAACCATATCACCATGTGGACGGACCCACTGAGATCTACAAGTTGACCC  
GCAAGAGGCGCCAGGAGTAGGAGGCTGCAGCGCCCGGCTGGGACGGTCTCTCCATACCCGAGC  
CCCTCTAAGTAGAGTGGGGAGCATGCCAGAGAGAGCTCAATGTACAAATGAATGCCTCATGGC  
TCTTAGCTGTGGTTTCTTGGACCAGCGGCATGGACATTTGTCAAGTTTGCCCTTCTGACGGTAGC  
TCTTGGAGGAAGATTCTCGCAGCCACTAATGCATTTGTATGATGATAACCAAAACTCTGGTATGA  
CACATTTTCTGTGATCATTTGTAATTAGTGACATAGTAACATCTGTAGCAGCTGGTAGTAAA  
CCTCATGTGGGGGTGGGTGGGGGTGTATTCTTGGGGATGGTTTGGGCCGAATGGGGAGTG  
GAATATTTGACATTTTCTGTTTAAATTTAGATAGATTTAAACATCCTTGGGGTCCCA  
GTCCAAGGTAGGCTGGTGTCAATAGTCTTCTCACTCCTAATCCATGACCACGTGTTCCTTCTTA  
TTTATATCACCAGGTAGCCTACTGAGTTAATATTTAAGTTGTCAATAGATAAGTGTCCCTGTT  
TTGTGCGCATAAATAAAGCAATTTTCATGAGAAGATTTATCCACAGGGGTATTTGACGTTTG  
AAACCAATCTGTATATCTAATACTAACCAATCTGTTGGATGTGGATTTTAAAAAATGTTTGC  
TAAACTACCCAGTAAGATTTACTGTATTAATAGCCTTCCGGGTCTGAAAAGCTTTTTTAACC  
TCTTGCTAAAAATCGCTTTTATTGATAAGATACCTTCAATAGCCPTCCAAAAGTGTAGATCC  
AATCACTTAAATAAACCTGTATGTATATGCAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 14**

MAGAIENMSTKKLCIVGGILLVFQIIAFLVGGLIAPGPTTAVSYMSVKCDARKNHHKTKWF  
VPWGPNNHCDKIRDIEEAI PREIEANDIVFSVHIPLPHMEMSPWFQFMLFILQLDIAFKLNNQI  
RENAEVSMDVSLAYRDDAFAEWTEMAHERVPRKLKCTFTSPKTPEHEGRYYECDVLPFMEIGS  
VAHKFYLLNIRLPVNEKKKINVGIGEIKDIRLVGIHQNGGFTKVWFAMKTFLTSPSIFIIMVWY  
WRRITMMSRPPVLEKVI FALGISMTFINIPVEWFSIGFDWTWMLLFQDIRGGIFYAMLLSFW  
IIFCGEHMMQHERNHIAGYWKQVGPIAVGSFCLFIFDMCERGVQLTNPFYSIWTTDIGTELA  
MAFIIIVAGICLCLYFLFLCFMVQVFRNISGKQSSLPAMSKVRRRLHYEGLIFRFKFLMLITLA  
CAAMTVIFFIVSQVTEGHWKGGVTVQVNSAFFTGIYGMWNLYVFALMFLYAPSHKNYGEDQS  
NGDLGVHSGEELQLTTTTITHVDGPTEIYKLTRKEAQE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**amino acids 239-253, 269-284, 302-318, 338-352, 377-399, 434-452,  
471-488**N-glycosylation sites.**

amino acids 8-12, 406-410

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 254-258

**N-myristoylation sites.**amino acids 223-229, 274-280, 305-311, 358-364, 374-380, 386-392,  
509-515

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**FIGURE 15**

GTGAGGGGAACAGCTGATCCGCTCTGTTGGGAGGACAGATATCTCAAGGCCAGG**ATG**GGAAGAA  
CACCCTAAGCCGGGCACCATCCCGTGGTGGAGTCAACTTCTCAATGTAGCCCGGACCTACA  
TCCCCAACCAAGGTGGAATGTCACTACACCCTTCCCCAGGCACCATGCCCGAGTCCAGGTG  
ACTGGATTGGCATTTTCAGGTGGAGGCTGCCTGTGTTCCGGGATTCACACACATTTGTGTGGT  
CTTCCGTGCCTGAAAGTACAACCTGATGGTCCCCCATTCACACCAGTGTCCAGTTCCAAGCCA  
GCTACTTGCCCAAAACAGGAGCTCAGCTCTACCAGTTCGGATATGTGAACCGCCAGGGCCAGG  
TGTGTGGGACAGGCCCTTCCAGTTCGGAGGCCAAGGCCCATGGTGAACCTGGTGACCC  
TGGAGGAGGCTGATGGGGGCTCTGACATCCTGCTGGTTGTCCCAAGGCAACTGTGTTACAGA  
ACCAGCTCGATGAGAGCCAGCAGAACGGAATGACCTGATGCAGCTGAAGCTACAGCTGGAGG  
GACAGGTGACAGAGCTGAGGAGCCGAGTGCAGGAGCTCGAGAGGGCTCTGGCAACTGCCAGGC  
AGGAGCACACGGAGCTGATGGAACAGTACAAGGGGATTTCGCCGTCCCATGGGGAGATCACAG  
AAGAGAGGGACATCCTGAGCCGGCAACAGGGAGACCATGTGGACCGCATCCTGGAGCTAGAGG  
ATGACATCCAGACCATCAGTGAGAAAGTGCTGACGAAGGAAGTGGAGCTGGACAGGCTTAGAG  
ACACAGTGAAGGCCCTGACTCGGGAACAAGAGAAGTCTCTTGGGCAACTGAAAGAAGTACAAG  
CAGACAAGGAGCAAGTGAAGGCTGAGCTCCAAGTGGCACAACAGGAGGAACCATCACTTAAATT  
TGGACCTGAAGGAGGCCACCTGGCAAGAGGAGCAGAGTGTCTCAGGCTCAGGCATGAAAG  
ACAAGGTGGCCAGATGAAGGACACCTTAGGCCAGGCCCAGCAGCGGTGGCCGAGCTGGAGC  
CCTTGAAGGAGCAGCTTCGAGGGGGCCAGGAGCTTGACGCTCAAGCCAGCAGAAAGCCACCC  
TTCTTGGGGAGGAGTTGCCCATGTCAGCAGCAGCCAGGACCCACCATAGCCCGACCTACACC  
GCAGCCGCTCGAAGTGGCTGAAGTTAACGGCAGGCTGGCTGAGCTCGTTTGCCTTGGAAGG  
AAGAAAAATGCCAATGGAGCAAGGAGCGGGCAGGGCTGCTGCAGAGTGTGGAGGCAGAGAAGG  
ACAAGATCCTGAAGCTGAGTGCAGAGATACTTCGATTGGAGAAGGCAGTTACAGGAGGAGGA  
CCCAAAACCAAGTGTTCAGACTGAGCTGGCCCGGAGAAGGATTCTAGCCTGGTACAGTTGT  
CAGAAAGTAAGCGGGAGCTGACAGAGCTCGGGTCAGCCCTGCGTGTGCTCCAGAAGGAAAAGG  
AGCAGTTACAGGAGGAGAAAAGGAATTTGCTAGAGTACATGAGAAAGCTAGAGGCCCTCGTGG  
AGAAGGTGGCAGATGAGAAGTGAATGAGGATGCCACCACAGAGGATGAGGAGGCCGCTGTGG  
GGCTGAGCTGCCCGGCAGCTCTGACAGACTCAGAGGACGAGTCCCCAGAAGACATGAGGCTCC  
CACCCTATGGCCTTTGTAGCGTGGAGACCCAGGCTCCTCTCCTGCTGGGCCCTGAGAGGCTT  
CTCCCTTGTGTGTCATCAGCCAGCCGGCTCCCATTTCTCCTCACCTCTCTGGGCCAGCTGAGG  
ACAGTAGCTCTGACTCGGAGGCTGAAGATGAGAAGTCACTCCTGATGGCAGCTGTGCAGAGTG  
GGGTTGAGGAGGCCAATTACTGCTTCTGAAGTGGGCAGTGCCCTTATGACATGGGCCAGTG  
GCTTTACAGTGGGTACCTGTGAGAACCAGCACTGGGGGCCCTGCCACCCCAATGGAAGG  
AGTGTCTCTATCTGTAAGGAGCGCTTCTCCTGCTGAGAGTGACAAGGATGCCCTGGAGACCACA  
TGGATGGACACTCTTTTTGACACCCAGGACCCCTTCACTTTGAG**TGA**TCTTACTCCCTCG  
TACATGCACAAATACACACTCATGCACACACACACTCACACATGCATAGCTAGGTTTCA  
TGCCCCATTTCTATCAACTCTGGGCTCCATGATATTTCTGTTCCCTAAGAATGCTTCTGTGTGC  
CCTGTTTTCTCCCAAGATTTCTCACTTCACTCCTCCTACCTGGCTCTTTGTGCCGGAG  
GGGTCTGTTCGGAAGCAGTGGCTGAATTTATCCCTGAAAGTGGTTTGGAGGAACCGGGAT  
GGAGGAGGCCCTCCCCGTGGGAATAGAATCGTCCACTCCTAGCCCTTGGTGTCTCTGATACA  
CAGCCACTGCACACACACTCACACTCACACTCCCTGTCTGATGCCCAAAAGCCAAATTCCT  
GGGGACCCCTACCTCTCTTATTGGAGTTTCGTTGGTTTACCTGAGTTTCTCTGGGGTCT  
GCACAGAGGCAGCAGCATGGACATCATGGCTCTCAGTCCCTTTGGTTTCTCAGTTTCAATTG  
GTCTCTCTTCTGTTCCTCCATTTGACTTCTGTGCCACCCTAGCCCTTTTCCATAACCTTAGG  
TATTCAGTTTGGAGGGGTTTTTGTATTTTGGAGGATTCCTGTATTCGTATCCTCTCCTCGC  
ATCTCCTCACATGGAAGAAATATGATTTTGTGCCTTCTGTAGGAATGGGGGAACAGAGTG  
GTCCAGGATATCCCCATTTCCAAGGCCCCCTCCTCTCCAGGTCCCCCACAGCAATAAAG  
CTTCCCCCTGATATCCATCCCTTTGTAGTTTGAACAAATATATTTATATGATATGAA



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**FIGURE 16**

MEESPLSRAPSRGGVNFNLNARTYIIPNTKVECHYTLPPGTMPASDWIGIFKVEACVRDYHT  
FVWSSVPESTTDDGSPIHSTSVQFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFREPRMDE  
LVTLEEADGGSDILLVVPKATVLQNQLDESQQERNLMLQLQLEQVTELRSRVQELERALA  
TARQEHTELMEQYKGISRSHGEITTEERDILSRQQGDHVARILELEDDIQTISEKVLTKVELD  
RLRDTVKALTRQEKLGLQKEVQADKEQSEAELQVAQQENHHLNLDLKEAKSWQEEQSAQAQ  
RLKDKVAQMKDRTLGAQQRVAELEPLKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIA  
ELHRSRLVAEVNGLRAELGLHLKEEKCQWSKERAGLLQSVEAEKDILKLSAEILRLEKAVQ  
EERTQNQVFKTELAREKDSSLVLQSESKRELTELRSALRVLQKEKEQLQEEKQELLEMYMRKLE  
ARLEKVADEKWNEDATTEDEEAAVGLSCPAALTDSEDESPEDMRLPPYGLCERGDGSSSPAGP  
REASPLVVISQPAPIPSHLSGPAEDSSSDSEAEDEKSVLMAAVQSGGEEANLLLPELGSAFYD  
MASGFTVGTLSSETSTGGPATPTWKECPICKERFPAESDKDALEDHMDGHFFFTQDPFTFE

**Important features:****Casein kinase II phosphorylation sites:**

amino acids 28-31, 43-46, 68-71, 72-75, 129-132, 156-159, 208-  
211, 239-242, 282-285, 305-308, 376-379, 383-383, 468-471, 520-  
523, 521-524, 537-540, 539-542, 543-546, 593-596, 595-598, 597-  
600, 612-615, 639-642, 652-655, 667-670, 683-686

**N-myristoylation sites:**

amino acids 39-44, 107-112, 204-209, 414-419, 561-566, 613-618

**Cell attachment sequence:**

amino acids 557-559

**Leucine zipper pattern sequence:**

amino acids 163-184, 475-496, 482-503

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**FIGURE 17**

GCAAGTTGGGAATTTAGACTGTCACATGGACCTCTGGGAAGACGTCTGGCGAGAGCT  
AGGCCCACTGGCCCTACAGACGGATCTTGCTGGCTCACCTGTCCCTGTGGAGGTTCCCCTGGG  
AAGGCAAGATGCCCAACAACAGCACTGCTCTGTCTATTGGCCAATGTACCTACATCACCATGG  
AAATTTTCATTGGACTCTGCGCCATAGTGGGCAACGTGCTGGTCATCTGCGTGGTCAAGCTGA  
ACCCAGCCTGCAGACCACCACCTTCTATTTTCATTGTCTCTCTAGCCCTGGCTGACATTGCTG  
TTGGGGTGCTGGTCAATGCCTTTGGCCATTGTTGTACGCTGGGCATACAATCCACTTCTACA  
GCTGCCTTTTTATGACTTGCCCTACTGCTTATCTTTACCACGCTCCATCATGTCTTGCTGG  
CCATCGCTGTGGACCGATACTTGCGGGTCAAGCTTACCGTCAGATTGAGAATTCCTGGGCTCC  
CTGGGTGCATTCTATCATTCAGTTGAAAGTTTGCTTCCTTCCAGTCATGTGGCTCTTCATTC  
TACTCTCCTTGGCTCTCATTTTCCAGATGCCATGGTCATGGATGAAAAGGTCAAGAGAAGCTTTG  
TGCTGGACACGGCTTCTGCCATCTGCAACTACAATGCCCACTACAAGAATCACCCCAAATACT  
GGTGGCGAGGCTATTTCCGTGACTACTGCAACATCATCGCCTTCTCCCCTAACAGCACCAATC  
ATGTGGCCCTGAGGGACACAGGGAACCAGCTCATTGTCACTATGTCTGCTGACCAAAGAGG  
ACACGGGCTGGTACTGGTGTGGCATCCAGCGGGACTTTGCCAGGGATGACATGGATTTTACAG  
AGCTGATTGTAAGTACGACACAAGGAACCCCTGGCCAATGACTTTTGGTCTGGGAAGACCTAT  
CAGGCAACAAAACAGAAAGCTGCAAGGCTCCCAAAGTTGTCCGCAAGGCTGACCGCTCCAGGA  
CGTCCATTCTCATCATTTGCATACTGATCACGGGTTTGGGAATCATCTCTGTAATCAGTCATT  
TGACCAAAAGGAGGAGAAGTCAAAGGAATAGAAGGGTAGGCAACACTTTGAAGCCCTTCTCGC  
GTGTCTGACTCCAAAGGAAATGGCTCCTACTGAACAGATGTGACTGAAGATTTTTTTAATTT  
AGTTCATAAAGTGATGCTACAACAGAATAATCACCATGACAACCTGGCCACACCTCAGAGACT  
GATTCTGATCTCCAGGAATTTGGAAGGACCTCTATCTTGACAACAATCATTTGCAGCCAG  
GTAGCAACGGCGGTAGTCAGAGGAGCTATGATAGACCACACCAAGCAAGGCTGCCCTCAAAT  
AACATCTCAAGATCTTAGTTCTTATGCATCCATCAGTCAGAAGTGAAGAAGAGGTGGAGAAT  
CTGGATTGGGGACAGGAAATCACTTGTATTTTGTTAGCCAATAAATTCCTAGCCAGTGTGA  
ATGAAAAAAAAAAAAA

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**FIGURE 18**

MPNNSTALSLANVTYITMEIFIGLCAIVGNVLVICVVKLNPSLQTTTFYFIVSLALADIAVGV  
LVMLPLAIVVSLGITIHFYSCLFMTCLLLIFTHASIMSLAIAVDTRYLRVKLTVRFRIPGLPGC  
ILSFQLKVCFLPVMWLFILLSLALISDAMVMDEKVKRSFVLDTASAICNYNAHYKNHPKYWCR  
GYFRDYCNIIAFSPNSTNHVALRDTGNQLIVTMSCLTKEDTGWYWCGIQRDFARDDMDFTELI  
VTDDKGTLANDEFWSGKDLGNGKTRSCAPKVVRKADRSRTSILIICILITGLGIISVISHLTK  
RRRSQRNRRVGNTLKPFSRVLTPEMAPTEQM

**Important features of the protein:****Transmembrane domains:**

amino acids 16-35, 62-80, 89-101, 134-152, 292-311

**N-glycosylation sites.**

amino acids 3-7, 4-8, 12-16, 204-208, 273-277

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 316-320

**N-myristoylation sites.**

amino acids 122-128, 125-131, 258-264

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 214-225

**G-protein coupled receptors proteins.**

amino acids 29-59, 76-116

FIGURE 19

TCGGGCGGCGCAGGCACTCTGGTTTGGCCCTGCATATTAGACTTCGGGCTCGCGCGGGGCGCGCCCTCTCCAATT  
 SCATATGTGTGTGGCTTGGAGCGAGCGCGCAAGCTTTCCGCAAAAGCACTCAGTGTGTGTTCAGCAACCGGGGAGTC  
 CTCTGAAAGCAGATAAAAGAAACATTATTAACTGTCTACGAGGGAGCGGCCCGCGCGGGGCTGTGCGCACT  
 CCCCAGCGAATCATTGGCTCTCTCCAGCTCCGAGGAGGAGAGAAAGCGGAATTCACCTCG  
 TTTCAGGACAGTGGACCTGTGATGATGGCCCTCTGAATTTATCAGATATTGATTATTAGCATGCCCCCTGT  
 GTTTGTGTGTATCCACACACACAGCTGCACAAAGGCTCTGGCTGTCTCCCTCTCCTGTTTCCAGCTCTCTGGGCG  
 AATCCCACTACTGTTTCAACTCTCCGCGAGGCGCAGCAGAGCTGTGTCAAFTTCGCAATCGAGAGGAGAGG  
 ACAGGGGAAAAGAAACAAAGCAGACAGCACTTGAGACTCCCGACTCCCAAAAGAGAACCCAGCATCAGCAAAA  
 AAAAAGATATGGGCCCCGAGGCTGTGCTGTGTGTTCTGTCTCGCAACTGTGTTTCTCTGTGGGTGGAAAGT  
 GGGCTCTCTGTCCGCAACCGCTGTGAAGGAGCATTTACAGAGGACCGCAGGAACATCCGCGCCCAACATCATCC  
 GGCTGTACGCGAGCAGGACCATTTGCACTGGGTTCCATGCAAGTGTAAACAGCCGCGGCATCATGAGCG  
 GGGCGGGCGCACTTATCAACGGCTCTGTGACCAACCACTGTCTGCTCCCTCAAGCTCTCCATCTCATCTG  
 CAAGTACCTTCACACACCAACACCTTACACCAACATGAGAATGTCTTCCGCTCTCTGGCAGCAGCAGCA  
 GCGCGCACTTTTGGCGTGTACTTCAATGACACTGGCTACCGGACAGCTTTCTTCGGGAAGTATCTTAATGAATA  
 CAACGGCTCTCTACGTGCCACCGGCTGGAGAGGCTGGCTGGCACTCTTAAAACTCCGCTTTTAACTACTAC  
 CTGTGTGTGCGAAGCGGGTGAAGAGAGAGAGCGGCTCCGACTACTCAAGGATTACTTCACGATTACATCATACCAA  
 TGACAGCTGTGAGTCTTCTCCGACGCTCAAGAAAGATGTACCCGACAGGCACTCTCATGTGTACATCAGGCTGT  
 AGCCCCCAGGCTCTGAGGATTCAGGCCCAACAAATTATTCAGCTCTTCCAAAGTCATCTGACACATCAGCCG  
 GAGTACTCAACTACGGCCCAACCGGACAGCACTTGATATCTACGGCTACAGGGGCCCATGAGCCGCACTCCACAT  
 GGAATTCACCAACTCTCCAGCGAAGCGCTTGACAGCCTCATGTGGTGGAGACTCTCTGAGACATATTAA  
 CAACATGTGCTGTTGAGACGGGCGAGCTTGACAAACACATGTATGTATACACCGCCGCACTACGGTTACCAACCTGG  
 CAGTTTGGCTGGTGAAGGGAAATCCATGCCATAGCATTTGATACATCAGGTCCTGGTGTACGTGAGGGCGGC  
 CAACCTGGAAGCGGCTCTGTCAATCCCAACTCTGTCTCAAACTTACCTTGGCCCCCACTCTGCAATATGCG  
 AGGCTGAGACACTCTGCGGATATGGACGGAAATCCATCTCAAGCTCTGACAGCAGGAGCGGCGCTGAATCG  
 TTCTCACTTAAAAAGAGATGAGGCTTGTGGCGGACTCTCTTCTGGTGGAGAGGCGAAGCTGCTACAAAGAG  
 AGCAATACAGAGGTGGAGCGCCAGGAGGAGAACTTTCTGCGCAAGTGTCCAGCTGTGAAGAGAGCTGTGACGCT  
 TGCTGATGACAAAGGCTGCTGAGCAGCTGGGACAGAGTGGCAATGTGGGAGGACGCCAGGGAGCGGTGAAG  
 GCTCTCAATAGTGGAGGCGCCCTGTGAGCTGGCGGCGAGCAGAGCCCTTCCAACCTCTGTCGCAAGATCTACGG  
 CAGGCGCGCGAGGCTGCACCTGTGACCGGGGAGTACAAGCTCAGCTCAGCTCGCGCGAGCGGAAATAACTCT  
 CARGAAGAGATCAAGGCGAGCTATGTGTCGCGAGTCTGCTCACTCCGCTCAGTGGCCATCGAGTGTGAGCGAGGT  
 GTACCACTGTAGGCTGGGTGTGCGCGAGCCGCGAAGCTACAAGCGGCACTCGCAGGCGCGGCTGTGAGGA  
 CCAGATGACAGAGATGTGTGGGAGTTCACTGGGCACTGGAGGCTTCCGCACTACTCAGCGCCCAACCACTTAA  
 AOTGACACACTCGTGTACTACTTAGAAGACACACTCAGTGTGACATGCACTGTACAGTCCCTCGAGGCT  
 CTGAAAGACCAACAGCTGCACATGACCAAGATGTAAACCTCCAGAACAAATTAAAGACCTGAGGAAAGT  
 CCGAGTCACTTGAAAGAAACCGGCCAGAGAAATGTGACTGTCCAAATACTCACTACACCCAGGAGAGG  
 CGCGCTCAAGCAGAGGCTCAGTGTGATCTTTCAGGAGAGGGGCTCGAAGAGAGAGCAAGGTGTGGCTGTT  
 CGGGGAGCAGAGGCTCAAGAGAAATCTCGCAAGCTCTCAGCGGCTTCGAGACACACAGCATGTGCACTGTCT  
 AGGCTCAGCTGTCTACCCAGCACACCAAGCTCGGACAGCGGCTTTTGCACTAGCTGGGCGCTTCTGTGCT  
 CTGCAACAGCGCCAAACATACGTACTGGTGTGATGAGGACATCAATGAGACTCAAAATTTCTCTTCTGTGTA  
 ATTTGCAACTGGCTCTAGAGATTTTGATTCACACAGGACCTTACCAGCTGTAGTATGCTGATGACACACT  
 GGAAGGGATGTCTCAACCGACTACACGTACAGCTACGTAGGAGTGAAGAGCTCGAAGGGTTACAGACGTTGAA  
 CCCCGGACTCGAAGACCTGACCTGCTGTGAGGAGAGCTTATGACATACAGGCACTTTACGCTCGAAAGTGGCC  
 AGAATCGAAGAGACTTCTTCCAATCACTGGGACACTGTGGGAGGCTGGGAGGTTTAAAGAACACAGAGGT  
 GGAATCCAAAGACCTTAGAGGCTACCTGACTGCACAGGCAATAAAACACTTGGGTGTATTTCCAGCAGGC  
 TGTGCTATTGGCCAGAGGCGCTCGAAGAGCAAGCAAGCACTCTGACTCAACATGACATCTTSGAGATATAACA  
 CAGGAGCAGAGATAACTTCAGGAAGTCCATTTTGGCCCTGCTTTTGGTTGGATATACCTCACACAGTGCAC  
 AAAATGCATTTTTCGTATCAAAAGTACCACTAACCTTCCGAGAGCTCACAAAGGAAACGGGACAGAGCG  
 AGCGAGAGAGATTTCTTGGAAATTTCTCCAGAGGGGAAAGTCTTGGAAATTTTAACTATAGGGGAAAGCG  
 GCTCTTCTTAAATCTCTTATTTCTTGCTTGTTCACAAAGGAAGTACAAGAGACGACAGGACAGCTGTG  
 AGAGGCTGAAGAACGTCGAGAGCTTTGCAATAGCTCAGTAGACACAAAGAGATGACATTTCTACTAGCACTAT  
 AAACCTCGTTGGCTCTGAGAAAGCTGCCTTATGTATATGTGACTATTTACATGTATCAACATGGGAAT  
 TTTAGGGGAACCTAATAAGAAATCCCAATTTTCAGGAGTGGTGGTGTCAATTAACGCTCTGTGGCGCTGTAA  
 GAAAA

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**FIGURE 20**

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQRDRRNIRPNIIILVLTDDQDVELGSMQV  
MNKTRRIMEQGGAHFINAFVTTMCCPSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHESTR  
FAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSDYSK  
DYLTDLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITPSYNY  
APNPDKHWMRYTGFMKPIHMEFTNMLQQRKLQTLMSVDDSMETIYNMLVETGELDNTYIVYT  
ADHGYPHIGQFGLVKGKSMPEYFDIRVPFYVRGPNVEAGCLNPHIVLNIDLAFTILDIAGLDIP  
ADMDGKSILKLLDTERPVRNRFHLKKKMRVWRDSFLVERGKLLHKRDNDKVDAQEENFLPKYQR  
VKDLCQRAEYQTACEQLGQKWQCVEDATGKCLKHKCKGPMRLGGSRALSNLVPKYYQGSEAC  
TCDSDGYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVLGLDAAQPRNLTKRHW  
PGAPEDQDDKDGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCDDLYKSLQAWKDHKLH  
IDHEIETLQNKIKNLEVRGHLKKRPEECDCHKISYHTQHKGRCLKHRGSSLHPFRKGLQEKD  
KVWLLREQKRKKKLKRLKLNNDTCSMPGLTCFTHDNQHWQAPFWTLGPFCACTSANNNNT  
YWCMTINETHNPLFCFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQLHVQLMELRSCKGY  
KQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

**Important features:****Signal peptide:**

amino acids 1-17

**Sulfatases signature 1.**

amino acids 86-99

**Homologous region to sulfatase:**

amino acids 87-106, 133-146, 216-229, 291-320, 365-375

**N-glycosylation sites.**amino acids 65-69, 112-116, 132-136, 149-153, 171-175, 198-202,  
241-245, 561-565, 608-612, 717-721, 754-758, 764-768

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**FIGURE 21**

GGGCGCGCAGAGAGCTGCTAGGGCGGTTTCTCTGCCTCGGGCCTGTTGGGCAGGGCCGGCT  
AAGGTGCGCGTGCTCGTGGTTCTAACCCTTCTGTTGGGCGTTTCTGCTGAGAGGCGGGA  
GGCGCTGAGAGTCTGTGCGGAGGTCCGTGGACAGACTGCTTTGCTCGTTGTTGCTCTTCG  
GAGGGCGCGATCCCCGAAGGCGAGCTGAAATACGGCTGCAGGCTACAATTTGCAGCCGAC  
GATTATGGAAGACGGAAGCGGGAGAGGTGGCCACCCTCATGGAGCGCTTGTGCTCGGAT  
GGCTTCGCATTTCCCAATACCCATTAAACCGTATCATCTGAAGAGGATCCACAGAGCT  
GTCTTACATGGTAATCTAGAGAACTGAAGTACCTTCTGCTCACGTATTATGACGCCAAT  
AAGAGAGACAGGAAGGAAGGACCGCCCTACATTTGGCCTGTGCCACTGGCCAACCGGAA  
ATGGTACATCTCCTGGTGTCCAGAAGATGTGAGCTTAACCTCTGCGACCGTGAAGACAGG  
ACACCTCTGATCAAGGCTGTACAAC TGAGGCAGGAGGCTTGTGCAACTCTTCTGTGCAA  
AATGGCGCCAATCCAATATTACGGATTTCTTTGGAAGGACTGCTCTGCACTACGCTGTG  
TATAATGAAGATACATCCATGATAGAAAACTTCTTTCACATGGTACAAATATTGAAGAA  
TGCAGCAAGGTATAGGTCAACCAATGTTATTTTCAAACCTATCTGAAATGAATTTATTTTA  
ACATTGACACATGTAAGGTCATTTTTCATATTGGAAGCTCAAACATTCCTTGAATGA  
AAATATTTTGAAATGCCTTAAC TGCTAAGATTTTACTTTAAATATTGGAACTTTAAAG  
AAGCATTATAGGGAACAGCCTTTTTTCATGCACTTATGGTAAATAACTATAAAAACAAAT  
GAATTACAATAAATTTATAATTCATGACAAC TGAAATTTGGGAAAGGTAATAGTTAAGTGT  
TTTTCCACTAAATTACTTTTT

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**FIGURE 22**

MERLCSDGFAFPQYPIKPYHLKRIHRAVLHGNLEKLKYL LLLTYDANKRDRKERTALHLACAT  
GQPEMVHLLVSRRCENLNCREDRTPLIKAVQLRQEACATLL LQNGANPNITDFFGR TALHYA  
VYNEDTSMIEKLLSHGTNIEECSKV

**Important features of the protein:**

**N-glycosylation site.**

amino acids 113-117

**N-myristoylation site.**

amino acids 109-115

**Microbodies C-terminal targeting signal.**

amino acids 149-153

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**FIGURE 23**

GAGGCAGAAAGGCAGAAAGGAGAAAAATTCAGGATAACTCTCCTGAGGGGTGAGCCAAGCCCTG  
CCATGTAGTGCACGCAGGACATCAACAAACACAGATAACAGGAAATGATCCATTCCCTGTGGT  
CACTTATTCTAAAGGCCCAACCTTCAAAGTTCAAGTAGTGATATGGATGACTCCACAGAAAG  
GGAGCAGTCACGCCTTACTTCTTGCCCTTAAGAAAAGAGAAGAAATGAAACTGAAGGAGTGTGT  
TTCCATCCTCCACGGAAGGAAAGCCCCCTCTGTCCGATCCTCCAAAGACGGAAAGCTGTGGC  
TGCAACCTTGCTGTGGCACTGCTGTCTTGCTGCCCTCACGGTGGTGTCTTTCTACCAGGTGGC  
CGCCCTGCAAGGGGACCTGGCCAGCCTCCGGGCAGAGCTGCAGGGCCACCACGCGGAGAAGCT  
GCCAGCAGGAGCAGGAGCCCCCAAGGCCGGCCTGGAGGAAGCTCCAGCTGTCAACCGGGGACT  
GAAAATCTTTGAACCACCAGCTCCAGGAGAAGGCAACTCCAGTCAGAACAGCAGAAAATAAGCG  
TGCCGTTTCAGGGTCCAGAAGAAACAGTCACTCAAGACTGCTTGCAACTGATTGCAGACAGTGA  
AACACCAACTATACAAAAAGGATCTTACACATTTGTTCCATGGCTTCTCAGCTTTAAAAGGGG  
AAGTGCCTTAGAAGAAAAAGAGAATAAAATATTGGTCAAAGAAACTGGTTACTTTTTTATATA  
TGGTCAGGTTTTATATACTGATAAGACCTACGCCATGGGACATCTAATTGAGGGAAGAAGGT  
CCATGTCTTTGGGGATGAATTGAGTCTGGTGACTTTGTTTCGATGTATTCAAATATGCCTGA  
AACACTACCAATAATTCTGTCTATTGAGCTGGCATTGCAAACTGGAAGAAGGAGATGAACT  
CCAACTTGCAATACCAAGAGAAAATGCACAAATATCACTGGATGGAGATGTCACATTTTTTGG  
TGCATTGAAACTGCTGTGAACCTACTTACACCATGCTGTAGCTATTTTCTCCCTTTCTCTGT  
ACCTCTAAGAAGAAAGAATCTAACTGAAAATACCAAAAAAAAAAAAAAAAAA



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**FIGURE 24**

MDDSTEREQSRLTSCLKKREEMKLKECVSILPRKESPSVRSSKDGKLLAATLLALLSCCLTV  
VSFYQVAALQGD LASLRAELQGHAEKLPAGAGAPKAGLEEAPAVTAGLKIFEPPAPGEGNSS  
QNSRNKRAVQGPEETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL EEEKENKILVKE  
TGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAK  
LEEGDELQLAIPRENAQISLDGDVTFFGALKLL

**Transmembrane domain:**

amino acids 47-72

**N-glycosylation site.**

amino acids 124-127, 242-245

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 33-36, 173-176

**N-myristoylation site.**

amino acids 96-101

**TNF family proteins.**

amino acids 172-206

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**FIGURE 25**

CTGCTTGGGATACCTCCAGTCCCCAAACTGTGTTCCAGGAGTTTTCTTGGCCGAAGCTGCCCGA  
TGTTTTGGCCTTTTCTTCCCAGAGAAGAAGATGGACTGAAAGCTGCCAGTTGGGGACTTTTGTG  
TGATCAGGGCGTTGCAGCGTTTTAAAGGAGGTGATGGGGCTTGCCTGGCTTGTCTTCCACC  
CAAGTGAAGAGTTGATGTTCTACTGGTATGCTTAGACAATGTGCAGTTTGGTTGTTAAAT  
TTTTGGGTGGGATAGGGGCATAGGCTTGTGAAGGGCAGTCCGGATCCGGAGGAATCGTCTTT  
GTCCTCGGTAGGAGAGACACCCCCAGTCTATCCTCGATGCCGTCAGCCTTGGCCATCTTCACT  
TGCCGCCCGAACTCGCACCCCGTTTCAGGAGCGTCATGTCTACCTGGACGAGCCCATCAAAATC  
GGCCGCTCAGTGGCCCGTGTGACACCAGCGCAGAATAATGCCACTTTTGATTGCAAAGTGCTA  
TCAAGGAACACGCTCTCGTCTGGTTTGATCACAAGACGGGCAAGTTTTATCTTCAAGACACT  
AAAAGTAGTAATGGTACTTTTATAAATAGCCAGAGATTGAGTCGAGGCTCTGGAAGAAAGTCCA  
CCATGTGAATTTCTTCCGGTGACATTATCCAGTTTGGAGTAGACGTGACAGAGAATACACGG  
AAAGTTACCCATGGGTGTATTGTTTCCACAATAAACTTTTTCTACCCAGATGGTATGGAGGCC  
CGGCTCCGCTCAGATGTCTATCCATGCACCATTACCAAGTCCTGTTGACAAAGTTGCTGCTAAC  
ACTCCAAGTATGTACTCTCAGGAACATTCCAGCTTTCTCAGTATCTACAGGAGGCCCTTACAT  
CGGGAACAAATGTGGAAACAGAAGTTAGCCACGCTTCAGCGGCTACTATGCCATCACCCAAGAG  
GCTTCAGATAGCAGTTGGACGCTTTAATAGATGAAGATAGACTCTTACCGTTAGAGGTT  
ATGGGAAACCAATTACAGGCATGCTCCAAAAATCAACAGAGAATAGTTTACGAAGGAAGCTT  
ATAGCATTACAAGAGGATAAACATAACTATGAGACAACGCCAAAGAGTCCCTGAGGCGGGTT  
CTTCAGGAGAAAAATTGAAGTGGTTAGAAAACTTTCAAGAGTTGAGCGAAGCTCGAGTAATACT  
GAAGATGAATGTACCCATCTGAAAGAAATGAATGAAAGGACTCAGGAAGAATTAGAGAAATTA  
GCCAACAAATATAATGGAGCAGTTAATGAGATTAAAGATTTATCTGATAAATTAAGAGTAGCA  
GAGGGAAAAACAAGAGGAAATCCAACAGAAAGGACAGGCTGAGAAAAAGAAATTACAACATAAA  
ATAGATGAATGGAAGAAAAAGAACAGGAGCTCCAGGCCAAAAATAGAAAGCTTTGCAAGCTGAT  
AATGATTTCCCAATGAAAGGCTAACAGCTTTACAAGTACGGTTAGAACATCTTCAGGAGAAA  
ACTCTTAAAGAAATGCAGCAGCTTGGCTGATCGTGAAGGGCCTCAACCAAGCGGTAGAAGA  
AACAAAGCTTTCAAAGGTTTGTGTTTCTGTTTTTCTATGTTTTTTGACAGTTCTTTTGGATAA  
TGAAGGTTAGTGTATATTTTCAAGGTTATAGTATTTTAAACATCAGTTTACTTCTTATAGCTC  
ACAAATAGCAAGGCCAGTAAACAGTATCAGATAATATATAAAATAATCAGACTCTCGTTTTAAG  
AAGGGTATCGTAACGTGAATGTGCTTTTTAAGTGGATGTAATTTATGGTTTTTGTGAATGTT  
AGTACTTCGATATAGGTTTCTTTAGGTATTAAAGATTTGTTGCAATCTCTGTCATTCCAGCAT  
ACTATTTCAGTTTGATCTCAAAATTTAATCAAAACACAATGTAAGTCGTTTGTGATACAACTTA  
AGTGAACATGCTTGCACCTTCTATTTTGGGGGTTACAGTACCTTTAAATCTCTTATGATGTT  
TAATATTTCCCTTAATTTTGGCAGTCTCAGTTTGATTTAAACAAAATTAATGACTTTTGTGAAT  
GTAGAATCTTCTTATATTTTATGAGTAGTCCAGTAATTGCCCAAAGTAGTTTATTGTGTTAAT  
TCTGTTACAGTTTGCAGAGAAGAAAAGTGAGTTTTAAAGCACCATATTGTCAAGTCACCTTTTA  
TACATAGGGAATTAGGCAAAATAAATTTGGTGGCATGTGTTTATCATAGTAGAAGCTTTTATTA  
GACTATACCAAGTATAAAATTTAAACTAGATTCCACAGTCCCTTTTGGCCAATTAAGCAATTGAG  
TTACAAAAGCTTTGAGATCACTAATTTTAGTACATTCTATTTTATTAAGTAACTGGATTCATT  
TGACTTTTTTAAACATGTAAGAGGATGGTGTATTTCAAATATCTCGTGGTTTCCATTCTCGAA  
TTTTGTGCACGGCAGATGCCATATTTGGGGAATAAATGCATAGAATATGCATCATTAATATTG  
TTTTGGCAACACGCATTGAGTTTTCAGAACAGTGAACATTTTTTAGTACATATGGCAATTTTT  
TTCACCTTATAAGTGTAGATGAGAACAGACCTTAAATAGCTTTTACCTCACCATCCAAATA  
CCTATTACAGATTAGTTGGTTGAATAGCCAGCACTTTGAAGTAGAGCCTTAGG

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**FIGURE 26**

MEARLRSDVIHAPLPSPVDKVAANTPSMYSQELFQLSQYLQEALHREQMLEQKLATLQRLAI  
TQEASDTSWQALIDEDRLLSRLEVGMGNQLQACSKNQTEDSLRKELIALQEDKHNYETTAKESL  
RRVLQEKIEVVRKLSEVERSLNTEDECTHLKEMNERTQEELRELANKYNGAVNEIKDLSDKL  
KVAEGKQEEIQQKGQAEKKELQHKIDEMEEKEQELQAKIEALQADNDFTNERLTALQVRLEHL  
QEKTLEKCSSLADRRRASNQSGRRNKAFKRFFVFCFSMFFDSSEFG

**Important features of the protein:****N-glycosylation sites.**

amino acids 98-102, 271-275

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 138-142, 267-271

**Amidation site.**

amino acids 273-277

**Tropomyosins proteins.**

amino acids 169-217

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**FIGURE 27**

GAACCTGGCGCCGCCGGAAGCTGATCGCGGCTAGTCCCAGCGTGTGTGCTAGTGAGCCGGA  
GCCGGGACGGCGGCAGTGGCGGCCCGGCTGCGAGGAGCCCGACGGGGTCTCTGCCATGGGGG  
AGTGACGCGCCTGCACCCGCTGTTCCGCGGCAGCGCGGAGACATGAGGAGACCCCGCGACAGG  
GGCAGCGGCGCGCGCTCGTGAGCCCGGGGATGGAGGAGAAATACGGCGGGGACGTGCTGGCCG  
GCCCGGCGCGCGCGCGGCCCTTGGGCCGCTGGACGTACCCAGCGCTCGATTAAACAAATATA  
TTGTGTTACTATGTTTCACTAAATTTTGAAGGCTGTGGGACTTTTCGAATCATATGATCTCC  
TAAAGCTGTTTCACATTGTTTCAGTTCATTTTATATTTAAACTTGGGACTGCATTTTATGG  
TTTTGTTTCAAAAGCCATTTTCTTCTGGGAAAATATTACCAACACCCAGTGGATCAAATAT  
TTAAACATGCAGTTGCTGGGTGTATTATTTCACTCTTGTGGTTTTTTGGCCCTCACTCTTTGTG  
GACCACTAAGGACTTTGCTGCTATTTGAGCACAGTGATATTGTTGTCATTTCACTACTCAGTG  
TTTTGTTCAACAGTTCTGGAGGAGGACCAGCAAAGACAAGGGGAGCTGCTTTTTTCATTATTG  
CTGTGATCTGTTTATTGCTTTTTTGACAATGATGATCTCATGGCTAAAATGGCTGAACACCCTG  
AAGGACATCATGACAGTGCTCTAACATCATATGCTTTACACAGCCATTGCCTTCTTAGGTGTGG  
CAGATCACAAGGGTGGAGTATTATTGCTAGTACTGGCTTTGTGTTGTAAGTTGGTTTTTCATA  
CAGCTTCCAGAAAGCTCTCTGTGCGAGCTGGTGGAGCTAAAGCTCTTCAAGCTTTATCTCATC  
TTGTTCTGTGCTCTCTCTGTCGCCATGGGCTATGTTCTTTCTGTGACAACTGAGAGTAAAG  
TGGAGTCTTGGTTTTCTCTCATATAGCTTTTGCACCGTTATCTTTTTTGTGTCATGATCTGG  
ATTTCTACGTGGATTCCATTTGTTTCAGTCAAAATGGAAGTTTCCAATGTGCTCGTTATGGAT  
CCTTTCCCAATTTTATTAGTGTCTCTCTTTTGGAAATTTTGGACACATCCAAACAGACC  
AGCTTCGGGCTATGAACAAAGCAGCACACCAGGAGAGCACTGAACACGTCTCTGTGCGAGGAG  
TGGTAGTGAGTGCTATATTCTTCATTTTGTCTGCCAATATCTTATCATCTCCCTCTAAGAGAG  
GACAAAAAGGTACCCCTTATTGGATATTCTCCTGAAGGAACACCTCTTTATAAATTTCATGGGTG  
ATGCTTTTCAGCATAGCTCTCAATCGATCCCTAGGTTTATAAGGAATCACTAAAACAAATTC  
TTGAGGAGAGTGACTCTAGGCAGATCTTTTACTTCTGTGCTGAACTGCTTTTTACCTTTG  
TGGAATTATTCTATGGCGTGCTGACCAATAGTCTGGGCTGATCTCGGATGGATTCCACATGC  
TTTTTGTACTGCTGCTGCTTTAGTCATGGGACTTTTTGCTGCCCTGATGAGTAGGTGGAAAGCCA  
CTCGGATTTTCTCTATGGGTACGGCCGAATAGAAATCTGTCTGGATTATTAATGGACTTT  
TTCTAATAGTAATAGCGTTTTTTGTGTTTATGGAGTCACTGGCTAGATTGATTGATCCTCCAG  
AATTAGACATTCACATGTTAAACACCACTCTCAGTTGGAGGGCTGATAGTAAACCTTATTGGTA  
TCTGTGCCCTTACCATGCCCATAGCCATGCCATGGAGCTTCTCAAGGAAGCTGTCACTCAT  
CTGATCACAGCCATTACACCATATGCATGGACACAGTGACCATGGGCGATGGTCACAGCCACG  
GATCTCGGGTGGAGGCATGAATGCTAACATGAGGGGTGATTTCTACATGTTTTGGCAGATA  
CACTTGGCAGCATTGGTGTGATCGTATCCACAGTTCTTATAGACAGTTTGGATGGTTTCATCG  
CTGACCCACTCTGTTCTCTTTCTACTGCTATATTAATATTTCTCAGTGTGTTCCACTGATTA  
AAGATGCCTGCCAGGTTCTACTCCTGAGATTGCCACCAGAATATGAAAAGAACTACATATTG  
CTTTAGAAAAGATACAGAAAATTTAAACATATGTCTGGCCTAAGTCTGGATTTTCATGATGTTCTGG  
ATTCTGCTAGTATTGTGGCAGGAACAATTATATACAGGTGACATCTGATGTGCTAGAACAAA  
GAAATAGTACAGCAGGTTACAGAAATACTTAAAGATGCTGGAGTAAACAAATTTAAACAAATTCAG  
TGAAAGAGGAGGCATCTTTCAACATATGTCTGGCCTAAGTCTGGATTTTCATGATGTTCTGG  
CTATGACAAAACAAATGGAATCCATGAAATACTGCAAGATGGTACTTACATCATGTGAGATA  
ACTCAGAATTACCCCTGGAGATAAACAATGAAGATTAAGTACTCAGTATGTTGTAATATTG  
CCAGAAGGATAAAATTAACATTTAACTGTACGAAACAGAGTTCCCTACTACTGGATCAAGG  
AATCTTTCTTGAAGGAAATTTAAATACAGAAATGAACATTAATGGTAAAAAAA

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**FIGURE 28**

MEEKYGGDVLAGPFGGGGLGPDVPSARLTQYIVLLCFTKFLKAVGLFESYDLLKAVHIVQFI  
FILKLGTAFFMVLQKPFSSGKTITKHQWIKIFKHAVAGCIISLLWFFGLTLCCPLRTLLEFE  
HSDIVVISLSSVLTSSGGGPAKTRGAFFIIAIVICLLLF'DNDDLMAKMAEHPEGHDSALTH  
MLYTAIAFLGVADHKGGVLLLVLALCCKVGFHTASRKLSVDVGGAKRLQALSHLVSVLLCPW  
VIVLSVTTESKVESWFSLIMPFATVIFVVMILDYVDSICSVKMEVSKCARYGSFFIFISALL  
FGNFWTHPTIDQLRAMNKAHQESTEHVLSGGVVSAIFFILSANILSSPSKRGQKGTLLIGYS  
PEGTPLYNFMGDAFQHQSSQSI PRFIKESLQKILEESDSRQIFYFLCLNLLFTFVELFYGVLTN  
SLGLISDGFHMLFDCCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGFINGLFLIVIAFFVF  
MESVARLIDPPELDTHMLTPVSVGGGLIVNLIGICAFSHAHSHAHGASQGSCHSSDHS SHHMH  
GHSDHGHGSHSGSAGGGMNANMRGVFLHVLADTLGSGIVIVSTVLIEQFGWFIADPLCSLSTA  
ILIFLSVVP LIKDACQVLLLRPFPEYEKELEHIALEKIQKIEGLISYRDPHFWRHSASIVAGTI  
HIQVTSQVLEQRIVQVVTGILKDAGVNNLTIQVEKEAYFQHMSSGLSTGFHDVLAMTKQMESMK  
YCKDGTIIM

**Important features of the protein:****Signal peptide:**

amino acids 1-46

**Transmembrane domains:**amino acids 59-77, 101-119, 150-167, 205-223, 239-258, 267-284,  
305-324, 343-360, 421-440, 452-469, 486-505, 522-539, 592-612,  
621-641**N-glycosylation site.**

amino acids 721-725

**Glycosaminoglycan attachment site.**

amino acids 143-147

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 225-229

**Tyrosine kinase phosphorylation sites.**

amino acids 750-758, 756-764

**N-myristoylation sites.**amino acids 14-20, 46-52, 102-108, 112-118, 144-150, 317-323,  
347-353, 369-375, 372-378, 437-443, 462-468, 529-535, 549-555,  
553-559, 579-585, 582-588, 583-589, 584-590, 605-611, 737-743**Multicopper oxidases protein:**

amino acids 561-569

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**FIGURE 29**

GGCACGAGGGCAGGATATTAGAAATGGCTACTCCCCAGTCAATTTTCATCTTTGCAATCTGCA  
TTTTAATGATAACAGAATTAATCTTGGCCTCAAAAAGCTACTATGATATCTTAGTGTGCCAA  
AATCGGCATCAGAGCGCCAAATCAAGAAGGCCTTTCACAAGTTGGCCATGAAGTACCACCTG  
ACAAAAATAAGAGCCCGGATGCTGAAGCAAAATTCAGAGAGATTGCAGAAGCATATGAAACAC  
TCTCAGATGCTAATAGACGAAAAGAGTATGATACACTTGGACACAGTGCTTTTACTAGTGGTA  
AAGGACAAAGAGGTAGTGGAAAGTTCTTTTGAGCAGTCATTTAACTTCAATTTTGATGACTTAT  
TTAAAGACTTTGGCTTTTTTGGTCAAAACCAAAACACTGGATCCAAGAAGCGTTTTGAAAATC  
ATTTCCAGACACGCCAGGATGGTGGTTCCAGTAGACAAAGGCATCATTTCCAAGATTTTCTT  
TTGGAGGTGGATTATTTGATGACATGTTTGAAGATATGGAGAAAATGTTTCTTTTAGTGGTT  
TTGACTCTACCAATCAGATACAGTACAGACTGAAAATAGATTTTCATGGATCTAGCAAGCACT  
GCAGGACTGTCACCTCAACGAAGAGGAAATATGGTTACTACATACACTGACTGTTCAGGACAGT  
AGTTCTTATTCTATTCTCACTAAATCCAACCTGGTTGACTCTTCTCTCATTATCTTTGATGCTAA  
ACAATTTTCTGTGAACATATTTTGACAAGTGCATGATTTCACTTTAAACAATTTGATATAGCTA  
TTAAATATATTTAAGGGTTTTTTTTTTTGACAAATTCACATTCAACGAGTAGACAAAATGCT  
AATTATTTCCCTGATTAGGAAAGTTCTTTAAAAAACACGTAATTTTGCCTAGTGCTTTTTTCT  
CTACCTGCCCTTGGGCTCACTAATATCACCAGTATTATTACCAAGAAAATATTGAGTTTACCT  
GATTAAACTTTAAAGTTAATTGTAGATTTAAATTGTGTGAACCTAATGATTTTGCAGTGAA  
ACCTTTACTAATTCAAAGTTGCATGTTCTATGACATCTGTGACTTGGCTTGACAGAGTGACAT  
GAAACTGTATAATTGAGTCATTAGTAAAGGAGAACAGTATCTTGGTTAATTGCTACTGAAAG  
GTTGAGAAAGGAATGGTTTATGATATTACCACAGCGCTGTGCCTTTCTACAGTAGAACTGGGGT  
AAAGGAAATGGTTTTATTGCCCATAGTCATTTAGGCTGGAAAAAAGTTGAAAACCTTAACGAAA  
TATTGCCAAGAGATTGTTATGTGTTTGGTTCCAGCCTAAAAATGATTTTGTAGTGTGAAATC  
ATAGCTACTTACATAGCTTTTTTCATATTTCTTTCTTAGTTGTGGCACTCTTAGGTCTTAGTA  
TGGATTTATGTGTTTGTGTGTGTAGTTTATCTCTCTCTCATCTTTATCTAGAGATTGACT  
GATACCTCATTTCTGTTTGTAACCAGCCAGTAATTTCTGTGCAACCTTACTATGTGCAATAT  
TTTTAAATCTGAGAAATGTGTGCTTTTGTFTTCGGATAGACTATTCTTTAGTTCTGCACT  
TTTCCACATTATACTCCATATGAGTATTAATCCTATGGATACATATTAACAAGTGTCTCAT

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**FIGURE 30**

MATPQSIFIFAICILMITELILASKSYYDILGVPKSASERQIKKAFHKLAMKYHPDKNKSPDA  
EAKFREIAEAYETLSDANRRKEYDTLGHSFTSGKGQRGSGSSFEQSFNFNFDLFDKDFGFFG  
QNQNTGSKKRFEHFQTRQDGGSSRQRHHFQEFSFGGGLFDDMFEDMEKMFESFGFDSTNQHT  
VQTENRFHGSSKHCRTVTQRRGNMVTYTD CSGQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**Nt-dnaJ domain signature.**

amino acids 27-59, 66-90

**Glycosaminoglycan attachment site.**

amino acids 96-100

**N-myristoylation sites.**

amino acids 32-38, 99-105, 102-108, 126-132, 211-217

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**FIGURE 31**

AAAGTTACATTTTCTCTGGAACCTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTGG  
GCAGAAAGGAGGGTGCTTCGGAGCCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACAAT  
TCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCTGAG  
ATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCAAATG  
CAGACTTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTTCATGTGGTTTCTTCTACGCA  
TTGATTCCATGTTTGGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTCTCTGT  
CTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGAAACAGTG  
TACTATTCTGTCTGAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCTGGATCCCC  
AGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATCACGGCCACT  
GTGCCATACAACCTTCGTGTCTAGGGCCACATTGGGCTCACAGACCTCAGCCTGGAGCATCCTG  
AAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGATCACCAAAGAT  
GGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCGAGTTGAGTTCCTTGTGGCTAC  
TGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGGGGGTATTCCAGTG  
CACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGACATTCTGAAGGCC  
ATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAAGGAGAGGCCATTCCC  
CTGGTACTGGCCCTGTTTGCCTTTGTGGCTTCATGCTGATCCTTGTGGTCTGTGCCACTGTT  
GTCTGAAAAATGGGCCGGCTGCTCCAGTACTCCTGTTGCCCGTGGTGGTCTCCAGACACC  
TTGAAAAATAACCAATTCAACCCAGAAGTTAATCAGCTGCAGAAGGGAGGAGTGGATGCCTGT  
GCCACGGCTGTGATGTCTCCTGAGGAACCTCCTCAGGGCTGGATCTCATAGGTTTTCGGAAGG  
GCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACCATGAGGGGACAAGTTGTGTT  
TCTGTTTTCGCCACGGACAAGGGATGAGAGAAGTAGGAAGAGCCTGTTGTCTACAAGTCTAG  
AAGCAACCATCAGAGGCAGGGTGGTTGTCTAACAGAACTGACTGAGGCTTAGGGGATGTG  
ACCTCTAGACTGGGGCTGCCACTTGTCTGGCTGAGCAACCTGGGAAAAGTGACTTCATCCCT  
TCGGTCTAAGTTTTCTCATCTGTAATGGGGGAATTACCTACACACCTGTAAACACACACAC  
ACAGAGTCTCTCTATATATACACAGTACACATAAATACACCCAGCACTTGCAAGGCTAGA  
GGGAAACTGGTGACACTCTACAGTCTGACTGATTCAGTGTCTTCTGGAGAGCAGGACATAAATG  
TATGATGAGAATGATCAAGGACTCTACACACTGGGTGGCTTGGAGAGCCCACTTTCCAGAAT  
AATCCTTGAGAGAAAAGGAATCATGGGAGCAATGGTGTGAGTTCACTTCAAGCCCAATGCCG  
GTGCAGAGGGGAATGGCTTAGCGAGCTCTACAGTAGGTGACCTGGAGGAAGGTACAGCCACA  
CTGAAAAATGGGATGTGCATGAACACGGAGGATCCATGAACACTGTGTAAGTGTGACAGTGTG  
TGCACACTGCAGACAGCAGGTGAAATGTATGTGTGCAATGCGACGAGAATGCAGAAGTCAGTA  
ACATGTGCATGTTTGTGTGCTCCTTTTTTCTGTTGGTAAAGTACAGAATTCAGCAAATAAAA  
AGGGCCACCCTGGCCAAAAGCGGTAAAAA



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**FIGURE 32**

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAPEGT  
VYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECVDVTDITATVPYNLRVRATLGSQTSAWSI  
LKHFPNRRNSTILTRPGMEITTKDGFHLVIELEDLGPQFEFLVAYWRRREPGAEEHVKMVRSGGIP  
VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPVLALFAFVGFMILILVVVPL  
FVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation sites.**

amino acids 40-44, 134-138

**Tissue factor proteins.**

amino acids 92-120

**Integrins alpha chain proteins.**

amino acids 232-263

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**FIGURE 33**

GAGACACGCGAGCGGGGAGACCTCCAAGGCAGCGAGGCATCGGACATGTGTGACGACATCTGG  
GGCGCACATCCGTCGAGCCCCGAGGGGAGATTGCCGGAACAATTCAAACCTGGCATATTGATCT  
TGGGGGTGACTGTCCCTGGCCGGCTGTGCGGTGGGAGTGCAGTGTGCACTCGCTCGGAAGTG  
TGTGCCAGTGTGTATGTGTGTGCGGTGTGCGGCTCCCCCTTCCCCCTTTTCCCGTCGA  
GTGATGCACCTTGGAAATGAGAATCAGAGGATGGAAATAGTCTGGGAGGTGCTTTTCTCTTCA  
AGCCAAATTTTCATCGTCTGCATATCAGCTCAACAGAATTCAACAAAAATCCATGAAGGCTGGTG  
GGCATACAAGGAGGTGGTCCAGGGAAGCTTTGTTCAGTTCCTTCTTTCTGGGGATTGGTGAA  
CTCAGCTTGGAAATCTTTGCTCTGTGGGGAACCGGCAGTGCAGTCAACATAGAGACCAGTCA  
CATGATCTTCGACCCCTTTCTGACACCTCTTCGCATCAACACGGGGGCGAGGAAGGTCACTGG  
GACCATGTACAACACTGGAAGACAGTATCCCTTCGCCTGGACAAGGAGCACTTGGTCAACAT  
ATCTGGAGGGCCCATGACATACAGCCACCGGCTGGAGGAGATCCGACTACACTTTGGGAGTGA  
GGACAGCCAAAGGTCGGAGCACCTCCTCAATGGACAGGCCTTCTCTGGGGAGGTGCACTCAT  
CCACTATAACCATGAGCTATATACGAATGTCACAGAAGCTGCAAGAGTCCAAATGGATTGGT  
GGTAGTTTCTATATTTATAAAAGTTTCTGATTCATCAAAACCATTTCTTAATCGAATGCTCA  
CAGAGTACTATCAACAAGAATAACATATAAAATGATGCATATTTACTACAGGGGCTTAATAT  
AGAGAACTATTCACAGACCTCTAGTTTTCATCACTTACGATTCGATGACTCATCTCCACC  
CTGCTATGAGACAGCAAGTTGGATCATAATGAACAAACCTGTCTATATAACCAGGATGCAGAT  
GCATTCCTTGCCTGTCTCAGCCAGAACCAGCCATCTCAGATCTTTCTGAGCATGAGTGACAA  
CTTCAGGCCGTGTCAGCCACTCAACACCGCTGCATCCGACCAATATCAACTTCAGTTTACA  
GGGGAAGGACTGTCCAACAACCGAGCCAGAAAGCTTCAGTATAGAGTAAATGAATGGCTCCT  
CAAGTAGGGAACAAGCCAGAAGAATCCCACCTCAGTGAATGCTACAACCTGTGAATTGACG  
TAACCTAGAATGTCCCCCTTCTTGCTTCTCTCTCCTTCTTCCCCCAAGCCTCATTCATTCTT  
GGGATTGGCCCTTTTCTTCATGAAAGTGTCTGCGAAACCATGGCAGAGGAATACATCTCTCAC  
ACATACTCACAACACACACACAAGCACTTGACATACATACAACACATGCAACATACCTA  
CACACACACACTCTCTTACAACCTCCATCATGGGAAGTCAAGTTTCAGAAACAAAGTCTCAT  
TCATAAGAGGTCTTGAAGAAAAATAACCAAGTAACTGATTTCAATTTTGATACCGTTTTCTCT  
GAACTAATAAATCTACCAATGAGACTTTTTCAGCCTTTGTACATACAAAATTTCTTCCAAAGA  
GAGAGGAGAAAAATACAGCTCTGATGGCATCAAACGCACTTTGCATCAAGTAATTTAGATAGT  
GTCCTAGGATCCTTTGAGGGTGTGGTAGCAGGTGAGCAGGACAAAGTTGACCAAGGACACTT  
ATTTCTAGATTATGATTCTTCTGTTTACTCAACAATTTACAAGAAAAAAGGACAGACATTG  
AAGAGCTACACATTGATATATATACCCACAGACTATAAGGAAATGGAATTAATTTCCCTCTT  
GTCACATATCTGTAGTAGGATTTGCCAAGATCAGAAATGATCCATTTGCTGTTTCTGTTTTC  
CAAAGGTATACATTGTGTTTGGTTATTGTTTACCAGCTCAATAAATGTGTTTAAACAGTTAAAT  
TTCATTTTCTGGCTTTGGTCTGTTCTCCTTCTACAGGCTAAGCCCTGGCTGCATGCAAT  
GCATTCCTTTGATTTCACTTGTTCCTTCATCTACATGTTTGTTCATTGTGACGCCAGTTTTCAT  
TGAGTTTGTGGCAATCAGGAATGCATTTGCTAAGCAAGTATGACTTTAATTCACCTCCATGGC  
TGAATTTGACATGAGGTGAGCTTCAGCCTGAGATAGCAGGGACAGACTTCTTGCCTTCA  
AACTGCCATGCCCCCCCTGTGATGCTCCCGTGAAGGAATGCATTTGCCCTTGAAGTCTCCGG  
GAAAGGGGTATGTTTCTCTCCAGGTGCAGCCAGATCTCACAAAGTACAAACGAATGCCCTT  
CTTTCTTGTTTATAATGTCCTACTCTGTTTGGTTACTGTCAAGAAATCAATAAATGTGT  
TTAACAAGTTA

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**FIGURE 34**

MEIVWEVLFLQLQANFIVCISAQQNSPKIHEGWWAYKEVVQGSFVPVPSFWGLVNSAWNLC SVG  
KRQSPVNIETSHMIFDPFLTPLRINTGGRKVS GMTMYNTGRHVSRLDK EHLVNI SGGPMTYSH  
RLEEIRLHF GSEDSQGSEHLLNGQAFSGEVQLIHNHELYTNVTEAAKSPNGLVVVSI FIKVS  
DSSNPFLNRMLNRDTITRITYKNDAYLLQGLNIEELYPETSSFIT YDGSMTIPPCYETASWII  
MNKPVYITRMQMHSRLRLLSQNQPSQIFLSMSDNFRPVQPLNNRCIRTNINFSLQ GKDCPN NRA  
QKLQYRVNEWLLK

**Important features:**

**Signal peptide:**

amino acids 1-20

**Eukaryotic-type carbonic anhydrases proteins.**

amino acids 126-162, 220-269, 43-91

**N-glycosylation sites.**

amino acids 116-119, 168-171, 302-305

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**FIGURE 35**

GTCGGAACCCCTCAGGCCACCCCTCGGGAGTCTGGGGTCCAGAGGGGTGTCCCTGTACCCCTTGACAC  
 ACAGGAGCCCTCACTCTGAGGGGATAGCCAGCTGCGCCTGCAGCCTAGGGGTGCCAAGGAGGGCTGCTGA  
 TTGTGGCCACAGCCCTCATCTGAACGCCAGGAGACCAGGATACCGAGGCCAGGGATCCCTCTCTGTG  
 CCTGGGGAGCCCAAGTGTCTGCCAGTACCCAGGGCTGAGGTCTGCGCTCCCTAGTGGTGAAGGCC  
 TGGTAGGACCGGGGACGGGAATGTAGCGCCATCCGAGCTCAGCGTTCTCTGAGTCCGCGGCTTCGT  
 GACTTTGGCAGGGGCTCGGGACAGTGAACCCAGTCAAAACCCAGAGGGTCTTGGCGCGCAGCAGCA  
 AGGAGGTATTAGGCTCCAGGCCAGGTGGGGCCGAGCGCCCCAGCCATCCACCAGTGGTGGTGGCACA  
 CCCCACCGCACTGCCACCACCACGCCCACTGCCACTGTACGGCCACCGTTGTGATGACCACGGCCA  
 CCATGGACCTGCGGGACTGGCTGTTCTCTGTCTACGGGCTCATCGCTTCTGACGGAGGTATCGAC  
 AGCACCACCTGCCCTCGTGTGCGCTGCGACAACGGCTTCATCTACTGCAACGACCGGGGACTCAC  
 ATCCATCCCCGCAGATATCCCTGTATGACGCCACCCCTCTACCTGCAGAACACCATCAACACCG  
 CCGGCATCCCCCAGGACCTCAAGACCAAGGTCAACGTGCAGGTCTATCTACCTATACGAGAATGACCTG  
 GATGAGTTCCCCATCAACTGCCCGGCTCCCTCCGGGAGCTGCACCTGCAGGACAACAAATGTGCGCAC  
 CATTTGCCAGGGACTCGCTGGCCCGCATCCCGCTGCTGGAGAAGCTGCACCTGGATGACAACCTCGTGT  
 CCACCGTCAGCATTTAGGAGGACGCTTCGCCGACAGCAACAGCTCAAGCTGCTCTCTCTGAGCCGG  
 AACCTCTGAGCAGCATCCCTCGGGGCTGCCGACACGCTGGAGGAGCTCGGGCTGGATGACAACCG  
 CATCTCCACATCCCGCTGCATGCCCTCAAGGGCTCAACAGCCTGCGCGCGCTGGTGTGACCGGTA  
 ACGTCTGCGGCAACAGCGCATCGCCGACGACACCTTCAGCGCCTACAGAACTCAGACAGCTCTCG  
 CTGGTGGCAATTCCTGCTGGCCGCCACCCCTCAACCTGCCAGCGCCACCTGCGGAGCTCTACCT  
 GCAGGACAATGCCATCAGCCACATCCCTACAAACGCTGGCCAAAGATGCGTGAGCTGGAGCGGCTGG  
 ACCTGTCCAACAAACCTGACACGCTGCCCGCGGCTGTTCGACGACCTGGGGAACCTGGCCAG  
 CTGCTGCTCAGGAACAACCTTTGGTTTGTGGCTGCAACCTCATGTGGCTGCGGGACTGGGTGAAGGC  
 ACGGGCGCGCTGGTCAACGTGCGGGGCTCATGTGCCAGGGCCTGAGAAGCTCGGGGGATGGCCA  
 TCGAAGCATATCCGCGAGATTGACGAGTGTTTGAGACGGGCGCAGGCGCGCTGGCCAATGCG  
 GCTGCCAAGACCAGGCCAGCAACACGCTCTGCCACCAGCGCCAGGGTCCCTGTTTACCCCTCAA  
 GGCCAAAAGGCCAGGGCTGCGCCTCCCCGACTCCAACATTGACTACCCCATGGCCACGGGTGATGGCG  
 CCAAGACCTTGCCCATCCACGTGAAGGCCCTGACGGCAGACTCCATCCGACCTACGTTGGAAGGCCAG  
 CTCCCAGCTCTCTTTCCGGCTCAGTTGGCTGCGCTGGGCCAAGCCACGCCCTGGGCTCCATCAC  
 GGAGCATCTGGTGCAGGGGCAAGACAGAGTACCTGCTGACAGCCTGGAGGCCAAGTCCACTTCACTTACA  
 TCATCTGATGTGCACCATGGAGACCAGCAATGCCATGTAGCTGATGAGACACCCGTGTGTGCCAAG  
 GCAGAGACAGCCGACAGTATGGCCCTACACCCACATCAACCCAGGAGCAGACGCTGGCCCCATGGC  
 GAGCTGCCCTGGCGGGCATCATCGCGGGGACGTGGCTCTGGTCTTCTCTCTCTGGTCTGGGG  
 CCATCTGCTGGTACGTGACACAGGCTGGCGAGCTGCTGACCCGGGAGAGGGCTACAAACCGGGGAC  
 AGGAAAAGGATGACTATTATGGAGTCAGGACCAAGAGGATAACTCCATCTCGGAATCCGCGGCC  
 TGGGCTGCAGATGTGTCATCAACCCGTACCGCGAGGAGGAGTACGTGGTCCACACTATCTTCC  
 CTTCCAAAGCCGACAGCCTCTGCAAGGCCACACACCACTTTGGCTACGGCACCACGGGGGCTACCGG  
 GACGCGCGCATCCCGGACATAGACTACTCTACACATGATGCGCCGCTGACCCGGCTGCCCGCTCA  
 GCCCAGCTGCCCTGGCTGGCCATGTGGCTTTGCCAGCCTGCTGCAATCCAAGAGACAGGAAGA  
 GAAATTCATGGGTGACTTTCTCCGAGAAAGCAAGTTTGGGAGGGCTGACGATTTGTAGAACA  
 CAACGTGACAATTTTTTTTAAAGAATAGAAGGCAGGAGGGGAATTCGACATTGTTGAACATAA  
 TTTATACCAAGTTATGCGCAATTTGGGGAGGGAAGGACTAAAAATAATATGACAGCAGGGCTGGGTGG  
 GTTTTTTTTTTCCCCCTGAACTGGAAGGATACTACTGTACACATCTGTGGACACCTCATGCTCT  
 GTTCAAGGCCATCACAAGGAACCGCCAGGGAGAAGCAGCGGCTCTCAAAGCTCCACACGAGCTCTC  
 CGCCCACTGGCCACTGCTGGCGACCCGATGGAAGGTTTTAGGCTCTTCAACAAAGGAGAGGGAAG  
 AAAAGATCTTTTGGCTGGAGATATGGTCTGAAATCTCTCCCTGGCTTATPCCATACCATTTCCCT  
 TGCAGATTTCGGAACATAGGCACTTTCACTGATCTTTGAACAACTATGTAGTCGATTAATAAAAA  
 AAAACAACTTTTTTCTAGGCTGAAGCCCTCTTCAAGTTGCATGCACACCGCTCCGTAGAAGCCCC  
 GCGGAAGCGGTAGCTTTTCCCTGCCACCTGGAGGTGCATCTGTGCTGTCTATCCCTGTGCGGGTG  
 TCTCTAAGTACAGATGGGTAGATAGAGCCACATGCACGCTCTTACCCTCTCTTGTGGGTGAGTTCT  
 ACCATTTCTGACAATAGAAATTGTGAAGGTGTAAAAA

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**FIGURE 36**

MVVAHPTATATTTPTATVTATVVMTTATMDLRDWLFLCYGLIAFLTEVIDSTTCPSVCRCDNG  
FIYCNDRLTSIPADIPDDATTLYLQNNQINNAGIPQDLKTKVNVQVIYLYENDLDEFPINLP  
RSLRELHLQDNNVRTIARDSLARIPLEKLHLDNSVSTVSIIEEDAFADSKQLKLLFLSRNHL  
SSIIPSGLPHTLEELRLDDNRISTIPLHAFKGLNSLRRLVLDGNLLANQRIADDTFSRLQNLTE  
LSLVRNSLAAPPLNLP SAHLQKLYLQDNAISHIPYNTLAKMRELERLDLSNNNLTTLP RGLFD  
DLGNLAQQLLLRNNPWFCGCNLMWLRDWWKARAAVNVVRGLMCQGPEKVRGMAIKDITSEMDEC  
FETGPGGGVANAAAKTTASNHASATTPQGSFLT LKAKRPGLRLPDSNIDYPMATGDGAKTLAI  
HVKALTADSIRITWKATLPASSFRLSWLRLGHSPAVGSITETLVQGDKTEYLLTALEPKSTYI  
ICMVTMETS NAYVADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGAVALVFLF  
LVLGAICWYVHQAGELLTRERAYNNGSRKKDDYMESGTTKDDNSILEIRGPGLQMLPINPYRAK  
EEYVVHTIFPSNGSSLCKATH TIGYGTTRGYRDGGIPDIDYSYT

**Important features of the protein:**

**Transmembrane domain:**

amino acids 552-573

**N-glycosylation sites.**

amino acids 249-252, 305-308, 642-645

**Leucine zipper pattern.**

amino acids 182-203, 299-320

**Phospholipase A2 aspartic acid active site.**

amino acids 57-67

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## FIGURE 37

[illegible]

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**FIGURE 38**

MAEPGSHSHLSARVRRRTERRIPRLWRLLLWAGTAFQVTQGTGFELHACKESEYHYEYTACDS  
TGSRWVAVPHTPGLCTSLSDPVKGTCSFSCNAGEFLDMKDQSCKPCAEGRYSLGTGIRFDE  
WDELPHGFASLSANMELDDSAESTGNCTSSKWVPRGDYIASNTDECTATLMYAVNLKQSGTV  
NFEYYPDSSIIIEFFVQNDQCQPNADDSRWMKTTEKGWEFHVELNRGNVLYWRTTAFSVW  
TKVPKEVLVRNIIATGVAYTSECFPCPKPGTYADKQGSFCKLCPANSYSNKGETSCHQCDDPK  
YSEKGSSSSNVRPACTDKDYFYTHTACDANGETQLMYKWKAPKICSEDLGAVKLPAAGVKTH  
CPFCNPGFFKTNNSTCQPCPYGSYSNGSDCTRCPAGTEPAVGFEYKWWNTLPTNMETTIVLSGI  
NFEYKGMTGWEVAGDHIYTAAGASDNDFMILTLVVPGFRPPQSVMDATENKEVARITFVFETL  
CSVNCELYFMVGVNSRTNTPVETWKGSKGKQSYTYIIEENTTSFTWAFQRTTFHEASRKYTN  
DVAKIYSINVTNVMNGVASVYCRPCALEASDVGSSTSCPAGYYIDRDSGTCHSCPNTILKAH  
QPYGVQACVPCPGPTKNNKIHSLCYNDCTFSRNTPTRTFNYNFSALANTVTLAGGPSFTSKGL  
KYFHHTLSLCGNQGRKMSVCTDNVTDLRIPEGESGFSSKITAYVCOAVIIPPEVTGYKAGVS  
SQPVSLADRLIGVTTDMTLDGITS PAELFHLESLGIPDVIFFYRSNDVTQSCSSGRSTTIRVR  
CSPQKTVPGSLLLPGTCS DGTCDGCFHFLWESAAACPLCSVADYHAI VSSCVAGIQXTTYVX  
REFKLCSSGGISLPEQRVTICKTIDFWLKVGISAGTCTAILLTVLTCYFWKKNQKLEYKYSKLV  
MNATLKDCDLPAADSCAIMEGEDVEDDLIFTSKKSLFGKIKSFTSKRTPDGDFDSVPLKTS SGG  
PDMDL

**Important features of the protein:****N-glycosylation sites:**

amino acids 153-156, 390-393, 391-394, 404-407, 544-547, 576-579,  
672-675, 717-720, 947-950

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**

amino acids 15-18, 563-566, 709-712

**Casein kinase II phosphorylation sites:**

amino acids 42-45, 59-62, 81-84, 146-149, 168-171, 282-285, 331-  
334, 340-343, 431-434, 449-452, 465-468, 523-526, 557-560, 761-  
764, 780-783, 835-838, 860-863, 893-896, 949-952

**Tyrosine kinase phosphorylation sites:**

amino acids 50-56, 109-116

**N-myristoylation sites:**

amino acids 77-82, 88-93, 152-157, 268-273, 288-293, 320-325,  
400-405, 405-410, 414-419, 463-468, 599-604, 616-621, 634-639,  
644-649, 839-844, 874-879, 912-917, 916-921

**Amidation site:**

amino acids 707-710

**Cell attachment sequence:**

amino acids 162-164

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**FIGURE 39**

GGGAAGGGGTTCTGGGCTGCCGACAGGCACACAGGCCAGAGCTTCGTGGATACCTGCAGGGCCCC  
AAAGGTCCCTCCCTGTTTTGAAGAGTGAGTGATGGCTATGAGGTAGCGGCCAGGCTGATCACC  
CCTGCGTTGGCTGGAGGCCAGAATTCGTAAATCCTCGCCAAGTCTTTCTCCAGGCCACTGGTT  
AGCTCATCTCAGCCTCCCTCTGGGAGCATCAACACCAACATGGCAGAGGGGACTGCAGTGGTGT  
GCTTTGGACCTGTGTACCCACCAAGGCTAAAGGCAGAGCCAGTGACTTTGCGGGGGTCTCT  
TCTCTAGGATTATCTGTACTTCCCCTCTGTCTCTTTTACTACGGGAGATCGAGCTAGCTATA  
AGCCACCTTTCTTTTCATGAGAACCACACTAAATTGCAAAATTTATCCGACTGCTGGAGGAGGGC  
AGCAGGTTGAGATTATGTTGGCAGGAAGAATGTTGGCATTGATTGGCAGCGCAGGGGACGAGAG  
CTGCTTTGTGCTTTAAAGGAGCCAAGTTACACCCCTGTTTAAACCTGCCTTCAAAGGGACGACT  
CTGTAAGATTCTCTGCTACTTTATTCAGTTTGACACGATGCCCTTCACTACCTCCACCTGAGGTCC  
CGCCTTCCCTCTGCCATAGGAGTTTGATTCTACAAAGAAACCAACATCAGAAATACATCC  
AGCATGGCTGGAGAGCTCCGACCAGCCAGCCTGGTGGTCTCGCCAGGTCCCTTGCTCCAGCT  
TTTGAAGATTCTGCCAGGTCAACACTGGTCCCTTACCCTGCTGGGCCAGAGTGAGCCAGAA  
AAGTGGATGCTGCCCTTCAAGTGCTATCTCAGAGACCAGGATGGGCCATCCCCAGTCTCTGG  
AAATACGAGTTCCGGTGCTTGCACCCGGTAGCCTGGCTTCGCTGGAGCAGTACTCGGAGCAGCTG  
AAGGACATGTTGGCTCTTCTCTGGCTGCAGCTTCTCCCTGGAGGAGCTTGGAGGAAAGCG  
GGGCTCCCCAGAAAGAGACCCAGCAGGTACAGGCCAGGCGGGTGATACAAGACAACAGTGCTCT  
TGTGTTACCCATGCTGGCTTCTGCTGCCCTCTGGTGGTACAGTAGAGGCCCATTTCCAAAGGAC  
AAGCTGGAAGGGCTGGTGCGGGCTGCTGCTCCCTCGGAGGTGAGCAGGGGCAACCTGTTTCAC  
ATGGGGCAGCCAGAACTGTTGGGAATCAAAGAGCTTTCCAAACCTGCCTACGGGGATGCCATG  
GTGTTGCCCCAGGGGAGGTTCCAGTGTTCTGGCCTTCTCCGCTGACCACTCTCGGAGCTGTC  
AGCAGCTGTGAGAGCCCCACTGGCTTTTGCCAGCATCCCAGGTGACAGAGTTATGCACTGACCTG  
AAGGATGCAAGGCTCCACCTGGTTGCTCAACCCAGAGAGAATTCAGAGGTCCATCACATT  
TCCCAAGATCCTCTGCACTACAGCATCGCGTCAGTCTCTGCTTCTCAGAAGATCAGAACTA  
GAGTCTATGATCGGCATAGACCCAGGGAACCGGGGATTTGGGCACCTGCTCTGTAAGAGTAG  
CTGCTGAAGGCCTCTCTCTCGCTGTCCCATGCCCGCTCAGTGCTCATCACCACTGGGTTCCCC  
ACACATTTCAATCATGAGCCTCCAGAAGAGACAGATGGCCCAAGGAGCTGTTGGTCTGGTT  
GCCTTCTGACGGCTTTGGAGAAGGAGGTGCGCCATAATGCTTGAACAGAGAGCCTGGAAGTGG  
CACCAGAAGATTGTTGAAGATGCTGTTGAGCAAGGTGTTCTGAAGACGCAGATCCCGATATTA  
ACTTACCAAGGTGGATCAGTGGAAGCTGCTCAGGCATTCCTGTGCAAAAATGGGGAGCCCGCAG  
ACACCTAGATTGACCACTGGTGGCCATAGAGCGTGCCGGAAGAGCTGCTGATGGCAATTAC  
TACAATGCAAGGAAGATGAACATCAAGCACTTGGTTGACCCCATTGACGATCTTTTCTGTGCT  
CGGAAGAAGATTCTGGAATCTCATCAACTGGAGTGGGTGATGGAGGCAACGAGCTTGGGATG  
GGTAAAGTCAAGGAGGCTGTGAGGAGGCACATACGGCACGGGGATGTCATCGCCTGCGACGTG  
GAGGCTGACTTTGGCGTCATTGCTGGTGTCTTAACTGGGGAGGCTATGCCCTGGGCTGCGCA  
TCTACATCCTGTACTCATGTGCTGTCACAGTCAGTACCTGAGGAAAGCTGTTGGACGTCACCAAG  
AGGGCACCTGGAGATCAGGCCTGGACTCAGGCCCCCTCCGTCGGTCAATTAAGGAAGAAAAATG  
CTGGGCATCTTGGTGAGCACAAGTCCGGAGTGCGCTCTCGGGCATGCTGGGCATGGAGGTG  
GATGGGCTGCCCTTCCACAACACCCACGCGGAGATGATCCGAAGCTGGTGAGCTCACCACG  
GCACAGGTGTAAACCGTCCATGTTCCGTGTGAGCAGAGTCCCTACCAACGGGCAGGTCTGCATC  
CGGGAGAAATGCAGCTGCTTCTGGCGACAATCCTGCTAGTAAACACTGGTCTTCCGTGAGCA  
CGAACACTCGCCTGGCTGGGAAACTGCATGCCACTTTCTGGGAGGGTGTAGTGAGGCTGACC  
GTGGACAAAGGACAAACATTTCTCTGGGGCTTTTAACTTTTATTCTTAAGACTCTAAAGCGGT  
TGATTCTCAACCTCTTCTGAGCTGGGCTTCTCAGGCAACCCAGTGGTCTCTCATGAGAACTCT  
TCTCGACAGTTCTTATGCGGACACTTGTGAACAATTAAGTGCAGGCGAGGATGAGAAACA  
AACATTCCCAGGCCATGTAGGATAGGATACTCCAGACTCCAGTCATCTCCCCCATCCATGGT  
TTCTGTTACTCATGGTTTCAGTTACTCATAGCCAAGTGCAGACCGAAATACTAAATGAAAA  
TTTCAGAAATAACAACCTCTTAAGTTTTAAAAA



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**FIGURE 40**

MPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAGELRPASLVVLPRLAPAFERFCQVNTGPL  
PLLGQSEPEKWMMLPPQGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFLGCSF  
SLEEALKEAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCPLVVTMRPIPKDKLEGLVRACCSL  
GGEQQQPVHMGDPPELLGIKELSKPAYGDAMVCPPEVVPVFWPSPFLTSLGAVSSCETPLAFASI  
PGCTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSTIASVSASQKIRELESMIGIDPGNRG  
IGHLLCKDELLKASLSLSHARSVLITTGFPPTHFNHEPPEETDGGPPGAVALVAFLLQALEKEVAI  
IVDQRAWNLHQKIVEDAVEQGVLTQIPILTYQGGSVAAQAFLECKNGDPQTPRFDHLVAIER  
AGRAADGNYNARKMNKHLVDPIDDLFLAAKKIPGISSTGVGDGGNELGGMKVKEAVRRHIR  
HGDVIACDVEADFAVIAGVSNWGGYALACALYILYSCAVHSQYLKAVGSPRPGDQAWTQAL  
PSVIKEEKMLGILVQHVKVRSGVSGIVGMEVDGLPFHNTHAEMIQLVDVTTAQV

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 358-378, 517-539

**N-glycosylation site.**

amino acids 28-32

**Tyrosine kinase phosphorylation site.**

amino acids 444-452

**N-myristoylation site.**

amino acids 98-104, 102-108, 123-129, 149-155, 181-187, 190-196,  
238-244, 308-314, 399-405, 413-419, 448-454, 477-483, 482-488,  
487-493

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 233-244, 531-542

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**FIGURE 41**

CTTTCCTGTTTTATCCGCAGCCCTTTTCTTCTTTGAGTTAGTAAAGATTTATTCTGTAACCTG  
ACACTCATCTGGCCCTTTGACGTTTGCCAGCCATATTCCCATGTGATTTCCCACTGGATCCAG  
GCCCCCATCCGGCTGGCAGGAGGGGGCTCTGACGTACAGGTTGGAAATCAGAAGTCTGTGAGA  
GCGCGGGAGTGCAATGGCAGCTCTGGGTCCCAGACCTGGCCCCGACCCCTCTGCTTCACCTCCAG  
CTCTGCTGCTCCTCTACTCTTGGGTCGAGATCCCTTTGGAGCCACAGCGAGGAACCCCTGTGGT  
CCTCAGGCAGGTGTACCTTGAGTCAGCCAGGAGCCCTCTTTTCTGTGTCAAAGCCTGCCCTC  
GGGCTCTGCTCACCTCTGGTGACCCCTCCAAGATGCCCCTGCCCTCAGTTTCCCCCTCATGATCT  
GGCCTCTGCCCCCTTCTCTAGCCACAGCCTCTAGTACACTTTAGCAATACCACCAGACTAGTT  
AGAGTTCCCCACTCACCAAGCAAGACAATGCAGTTTCATGCCTCTGTGCCTTCGCTCATGTGT  
TTCTTCCGACTGGAATGCCTTCCCCTGCTCCTCCTGCCTTGCTGCCTGGCAAGTTCATCTCT  
CACGATCCCCCTCAAAGGCCCCCTCCTCCAGGAAGGCAACCCCTGTGCCCCCTCCCCCTCCAGGCT  
ACCTCTGCACTTTTGTCAATGCTTCTCTTGTGGCACTTATCACACTGTATTTTACTTGTTTACA  
TGTTTGTCTCCCCCTTCTAGACTGTGAATCCTTAAGGGCATGGACTGTATCTTATGCATCTCTG  
TATTTCTGCGCCTAGCACGGTGCCTAGCACACAGTAGGCGCTCAATAAATGTTGAATGAATGA  
ATGATTT

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**FIGURE 42**

MQFHASVPSLMLFLEPTGMFSPAPPALSAWQVHLRSRSPQRPPPPGRQPLCPSPPGYLCTLSMLL  
LWHLSHCILLVYMFVSPSRL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-22

**Microbodies C-terminal targeting signal.**

amino acids 81-83

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**FIGURE 43**

GTTTCCAACAAGGATGATATGAAGACTTCCTCGAAGAAAGTTGTGAAGGGACCTCCTACGAGA  
**TG**ATGATGTCAGTGTGTGTCCCGCATGTTGGCCACCCCCCTGCATGTCATCTCAATGCGCTGCA  
TGGTCCAGTTTGTGGACGGGAGGCCAAGTACAGTGGTGTGCTGAGCTCCATTGGGAAGATTT  
TCAAAGAGGAAGGCTGCTGGGATTCTTCGTTGGATTAATCCCTCACCTCCTGGGCGATGTGG  
TTTTCTGTGGGGCTGTAACTGCTGGCCACTTCATCAATGCCTACCTGCTGGGATGACAGCT  
TCAGCCAGGCCCTGGCCATCCGGAGCTATACCAAGTTCGTGATGGGGATTGCAGTGAGCATGC  
TGACCTACCCCTTCTCTGCTAGTTGGCGACCTCATGGCTGTGAACAACCTGCGGGCTGCAAGCTG  
GGCTCCCCCTTACTCCCGAGTGTTCAAATCCTGGATTCACTGCTGGAAGTACCTGAGTGTGC  
AGGGCCAGCTCTTCCGAGGCTCCAGCCTGCTTTTCCGCCGGGTGTCATCAGGATCATGCTTTG  
CCCTCGAG**TAA**CCCTGAATCATCTAAAAAACCGGTCTCAACCTGGCCACTGTGGGTGAGGCCT  
GACCACCTTGGGACACCTGCAAGACGACTCCAACCCAACAACAACCAGATGTGCTCCAGCCCA  
GCCGGGCTTCAGTTCCATATTTGCCATGTGTCTGTCCAGATGTGGGGTTGAGCGGGGTGGGG  
CTGCACCCAGTGGATTGGGTCACCCGGCAGACCTAGGGAAGGTGAGGCGAGGTGGGGAGTTGG  
CAGAATCCCATACTTCGCAGATTTGCTGAGTCTGTCTTGTGCAGAGGGCCAGAGAATGGCTT  
ATGGGGGCCCAGGTTGGATGGGGAAAGGCTAATGGGGTCAGACCCCAACCCGCTCTACCCCTCC  
AGTCAGCCCCAGCGCCATCCTGCAGCTCAGCTGGGAGCATCATCTCTCTGCTTTGTACATAGG  
GTGTGGTCCCCTGGCACGTGGCCACCATCATGTCTAGGCCTATGCTAGGAGGCAATGGCCAG  
GCTCTGCCTGTGTTTTTCTCAACACTACTTTTCTGATATGAGGGCAGCACCTGCCTCTGAATG  
GGAAATCATGCACTACTCAGAATGTGTCTCCTCATCTAATGCTCATCTGTTTAAATGTTGAT  
GCCTCGCGTACAGGATCTGGTTACCTGTGCAGTTGTGAATACCCAGAGGTTGGGCAGATCAGT  
GTCTCTAGTCTACCCAGTTTAAAGTTCATGGTAAGATTTGACCTCATCTCCCGCAATAAA  
TGTATTGGTGATTGTGAAAAAAAAAAAAAAAAAAAA

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**FIGURE 44**

MMMQCVSRMLAHPHVISMRMVQFVGREAKYSGVLSSIGKIFKEEGLLGFFVGLIPHLLGDV  
VFLWGCNLLAHFINAYLVDDSFQALAIRSYTKFVMGIAVSMITYPFLLVGDLMVNNCGLQA  
GLPPYSPVFKSWIHCWKYLSVQGQLFRGSSLLFRRVSSGSCFALE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 51-72, 97-114

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 160-163

**N-myristoylation sites.**

amino acids 34-39, 100-105, 123-128, 165-170

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**FIGURE 45**

GCTCACTCTTTGGGTCCACACTGCCTTTATGAGCTGTAACACTCACTGGGAATGTCTGCAGCT  
TCACTCCTGAAGCCAGCGAGACCACGAAACCACAGGAGGAACAAACACTCCAGACGCGCAG  
CCTTAAGAGCTGTAACACTCACCGCGAAGGTCTGCAGCTTCACTCCTGAGCCAGCCAGACCAC  
GAACCCACCAGAAGGAAGAAACTCCAACACATCCGAACATCAGAAGGAGCAAACTCGTGACA  
CGCCACCTTTAAGAACCCTGACACTCAACGCTAGGGTCCGCGGCTTCATTCTTGAAGTCAGTG  
AGACCAAGAACCCACCAATTCGGGACACGGCAAAGTAACATCCTAGACATGGCTTTAGAGATC  
CACATGTGAGACCCCATGTGCCCTCATCGAGAACTTTAATGAGCAGCTGAAGGTTAATCAGGAA  
GCTTTGGAGATCCTGTCTGCCATTACGCAACCTGTAGTTGTGGTAGCGATTGTGGGCCTCTAT  
CGCACTGGCAAAATCCTACCTGATGAACAAGCTGGCTGGGAAGAAACAAGGGCTTCTCTGTTGCA  
TCTACGGTGCAGTCTCACACCAAGGGAATTTGGATATGGTGTGTGCCCTCATCCCAACTGGCCA  
AATCACACATTAGTCTCTGCTTGACACCGAGGGCTGGGAGATGTAGAGAAGGCTGACACAAG  
AATGATATCCAGATCTTTGCACTGGCACTCTTACTGAGCAGCACCTTTGTGTACAATACTGTG  
AACAAAATTGATCAGGGTGCTATCGACCTACTGCACAATGTGACAGAAGTACAGATCTGCTC  
AAGGCAAGAACTCACTGACCTTGACAGGGTTGAAGATCCTGCTGACTCTGCGAGCTTCTTC  
CCAGACTTAGTGTGGACTCTGAGAGATTTCTGCTTAGGCCTGGAAATAGATGGGCAACTTGTC  
ACACCAGATGAATACCTGGAGAATTCCCTAAGGCCAAAGCAAGGTAGTGATCAAAGAGTTCAA  
AATTTCAATTTGCCCCGTCTGTGTATACAGAAGTTCTTTCCAAAAAAGAAATGCTTTATCTTT  
GACTTACCTGCTCACCAAAAAAGCTTGCCCAACTTGAAACACTGCCTGATGATGAGCTAGAG  
CCTGAATTTGTGCAACAAGTGACAGAATTCTGTTCTACATCTTTAGCCATTCTATGACCAAG  
ACTCTTCCAGGTGGCATCATGGTCAATGGATCTCGTCTAAAGAACCTGGTGTGACCTATGTGTC  
AATGCCATCAGCAGTGGGGATCTGCCCTGTCATAGAGAATGCAGTCTTGGCCTTGGCTCAGAGA  
GAGAAGTCAAGTGCAGTGCAAAAGGCCATTGCCCTATGACCAGCAATGGGCGAGAAAGTG  
CAGCTGCCATGGAACCCCTCCAGGAGCTGCTGGACCTGCACAGGACCAGTGAGAGGGAGGCC  
ATTGAAGTCTTATGAAAACTCTTTCAAGGATGTAGACCAAGTGTTCAGAAAAGAAATGGAG  
ACTCTACTAGATGCAAAACAGAATGACATTGTGAACCGGAACCTGGAGCATCCTCGGATTAT  
TGCTCGGCTTTACTTAAGGATATTTTGGTCTCTAGAAGAAGCAGTGAAGCAGGGAATTTAT  
TCTAAGCCAGGAGGCCATAATCTCTTCAATCAGAAAACAGAAGAACTGAAGGCCAAAGTACTAT  
CGGAGCCTCGGAAGGAATACAGGCTGAAGAAGTTCTGCAGAAATATTTAAAGTCCAAGGAG  
TCTGTGAGTCATGCAATATTACAGACTGACCAGGCTCTCACAGAGACGGAAAAAAGAAAGAAA  
GAGGCACAAGTGAAGCAGAAGCTGAAAAGGCTGAAGCGCAAGGTTGGCGGCGATTCAAAGG  
CAGAACGAGCAAAATGATCAGAGAGAGGGAGAGACTCCATCAGGAACAAGTGAGACAAATGGAG  
ATAGCCAAACAAAATTTGGCTGGCAGAGCAACAGAAAAATGCAGGAACAACAGATGCAGGAACAG  
GCTGCACAGCTCAGCACAACTTCCAAGCTCAAAATAGAAGCTTCTCAGTGAGCTCCAGCAC  
GCCACAGGGCTGTTAATAACGATGATCCATGTGTTTTACTCTAAAGTGCTAAATATGGGAGT  
TTCCTTTTTTACTCTTTGTCACTGATGACACAACAGAAAAGAACTGTAGACCTTGGGACAA  
TCAACATTTAAATAAACTTTATAATTATTAA

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**FIGURE 46**

MALEIHMSDPMCLIEFNEQLKVNQEALEILSAITQPVVVVAIVGLYRTGKSYLMNKLAKGNK  
GFSVASTVQSHTKGIWIWCVPHPNWPNHTLVLLDTEGLGDVEKADNKNDIQIFALALLLSSTF  
VYNTVKNIDQGAIDLLHNVTETDCLKARNSPDLDRVEDPADSASFFPDLVWTLRDFCLGLEI  
DGQLVTPDEYLENSLRPKQGSQQRVQNFNLPRLCIQKFFPKKKCFIFDLPAHQKKLAQLETLP  
DDELEPEFVQVQVTEFCSYIFSHSMTKTLPGGIMVNGSRLKNLVLTYYVNAISSGDLPCIENAV  
ALAQRENSAAVQKAIHYDQQMGQKVLPMETLQELLDLHRTSEREAEVFMKNSFKDQVDSF  
QKELETLLDAKQNDICKRNLEASSDYCSALLKDI FGPLEEAVKQGIYSKPGGHNLFIQKTEEL  
KAKYYREPRKGIQAEVVLQKYLKSKESVSHAILQTDQALTETEKKKKEAQVKAEEKAEQRL  
AAIQRQNEQMQRERERLHQEQVRQMEIAKQNLAEQKMQEQMQEQAAQLSTTFQAQNRSL  
SELQHAQRAVNNDDPCVLL

**Important features of the protein:****Transmembrane domains:**

amino acids 31-49, 114-131

**N-glycosylation sites.**

amino acids 90-94, 144-148, 287-291, 563-567

**N-myristoylation sites.**

amino acids 45-51, 283-289

**Prenyl group binding site.**

amino acids 583-588

**ATP/GTP-binding site motif A (P-loop).**

amino acids 45-53

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**FIGURE 47**

CACTCATTTCATTCCAAAGGGTCTCTCAAGCAATGGTAATGTGCAAGGAGGTGATACCTAAAT  
GAATGACCAAAAGAACATGCTTCTGCTTTTGTGTGTCTCCTACATTTTAGACATTTGTTTGT  
TCTCTGGTAGCCTTTAAATTCCTTGAAGCCCAGGACCATGTCTCACTTACCTTTGTGTTTCC  
ACTAACTAGTCTACCTCCTGGAATTGGCAGATACTCAGTGAAGCCCTGTGAAATAAGTGATGT  
CTATTTCTAGCATATTATTCTGAGATTTAATGATAGATTTAGTGATTGAATGAGATTTCCATT  
TTCAAATACAGCAAAAGCATAACTATTTTCATTTCATTTCATTTCATTTCATTTCCTCAA  
ATTAGGTCCTGAGTTAACTAATAATTACCTTTGAAATGTGTGGGTATTTTGAGGCAATCAGGT  
GGTGACATTGAGCTCTCAGCCAGAGTTTGTCTTCTGGAATTGATTCAGTTCATTGCATTGATT  
TTTGTCTCAGAAGCCAAGGTTTCCCATGAAAAATCATTCCCACTTGAATTGGGCTGTGATTC  
TTGCTGCGTTTAAAGTAAAGGAAGCCTCTTGGTTCTAGTTCTGCAAACTTACACACTGAACTGG  
GACAAGTTTTTGTTTAGAGTAATGGCTGGGAAAAGAGGAACCTTTCATTTTATTGAGAAGTCA  
AAAACAAAGGCCTCCCAGCCACCTGGAGATGTTTTGTGTCAGACACCAGCCTGGCTCTGTCTT  
TATGCTTAACAATTGAGCATCCAGTCTTCTTTGTGCTGGGACCATTGCTCAGCTCTGCAAGGG  
GAAAAGAGGGAGAAAGCCAGAGCTGCCAGGCTTCTTGCACTGGGGCCGGGGGAGGGTTCTCG  
GAAGCAGGTGCTCTCTGGCTTCTTGGTACGTGAGGCTCTCGGAGCTGCCTCTCCTCTGACCT  
CAGGTCCTCACCGAGTTTGCTCCAGGAGTATATTGAAAACATACCCAGTGCTCTCTCAAGCAC  
CCACTGCTTAGAGGGCCAGATTTCTTTTCTTCTTTCCCTTGCAAGCTGGAGACTGCATCG  
GGCATCTGGTGTTTAAACTAAACAGGAAAACCTGACTAAAGGTCCACAGTGCTCATTGTGTAGA  
CTAGCTGCCCTCCGATGGTGTCTGATTATCAGTGGTTCAGTGAGGGCCTGTCACTAAAC  
AGGCCTCACTTCCTCCTTGGGGGCTTTCCCATGGGAGGTGTGGCTTTTTACTCTACATGGAAA  
TGACTCTCTGCAGCCACAGAACACAGTCATTTTCTGAATTATCCCACTCTCTCATGCGCCCTG  
GATTCTCCAGATGCCTTATATCTCTTGTGCAAAGTTGTCTAAAATTGGTTCCAGCTTCCA  
AGCCTTGCCCTTTTGCCCTTCTGGAAGTATTTTGTGTGATGAGTCGTCTGTCAATTATTCTCTA  
AAATGATTTGCTTTTGTCTTCTTTCATTCTATTTCCACCCACATATACACACATGCTCTT  
AACTTAGGGGATTACATGCCAATAAATCTATTGTTGAAAATGCACTAATACTATCGCAAAGAC  
GAAAATTACAGGCTGAACCGTTGTAAGTCCATATGCTCCTCAACTTACATGTGTGATGGAGT  
TATGCCCAATAAGTCCATCGTCAAGTTGAAAAATCAAATCAAGCCATCTTAGGTTGAGGAC  
CATTTGTTGTACCTCCAAGATGTCTATCTTTAAACATACTCCCTAGCTTTTCTTTTACT  
TTTTATTTTGAAGTAATTATAGAATCACAGAAAGTTGCAAAAAA